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152519

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CRFE

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 5-4-05  
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 0913404595  
Location (Bldg/Room#): 2D28 (Mailbox #): 2-18 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Compos + methods for Tumor Therapy

Inventors (please provide full names): POHARJER et al

Earliest Priority Date: 6-28-99

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

MEJ

Please search Seq ID No: 1

NA 2133 For interference + regular data  
loss.

No size limits. Zar 595  
5/6 5p

01 Thanks.

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: \_\_\_\_\_ NA Sequence (#) \_\_\_\_\_

\_\_\_\_\_ STN \_\_\_\_\_ Dialog

Searcher Phone #: \_\_\_\_\_ AA Sequence (#) \_\_\_\_\_

\_\_\_\_\_ Questel/Orbit \_\_\_\_\_ Lexis/Nexis

Searcher Location: \_\_\_\_\_ Structure (#) \_\_\_\_\_

\_\_\_\_\_ Westlaw \_\_\_\_\_ WWW/Internet

Date Searcher Picked Up: \_\_\_\_\_ Bibliographic \_\_\_\_\_

\_\_\_\_\_ In-house sequence systems

Date Completed: \_\_\_\_\_ Litigation \_\_\_\_\_

\_\_\_\_\_ Commercial \_\_\_\_\_ Oligomer \_\_\_\_\_ Score/Length  
\_\_\_\_\_ Interference \_\_\_\_\_ SPDI \_\_\_\_\_ Encode/Transl  
\_\_\_\_\_ Other (specify)

Searcher Prep & Review Time: \_\_\_\_\_ Fulltext \_\_\_\_\_

Online Time: \_\_\_\_\_ Other \_\_\_\_\_



Result No.	Query			ID	Description
	Score	Match	Length		
1	1000.2	46.9	2079	3	US-09-297-751-1
2	928.2	43.5	933	6	5340934-12
3	928.2	43.5	933	6	5340934-12
4	813.6	39.0	7375	3	US-09-513-442-1
5	731.6	33.5	844	4	US-10-000-489-19
6	469	22.0	481	4	US-09-640-173-190
7	469	22.0	481	4	US-09-713-550-190
8	469	22.0	481	4	US-09-825-294-190
9	469	22.0	481	4	US-09-970-966-190
10	450.4	21.1	460	4	US-09-640-173-189
11	450.4	21.1	460	4	US-09-713-550-189
12	450.4	21.1	460	4	US-09-825-294-189
13	450.4	21.1	460	4	US-09-970-966-189
14	428.4	20.1	490	4	US-09-513-998C-141
15	407.8	19.1	454	3	US-09-404-879A-179
16	407.8	19.1	454	4	US-09-338-933-179
17	407.8	19.1	454	4	US-09-215-681-179
18	407.8	19.1	454	4	US-09-216-003A-179
19	407.8	19.1	454	4	US-09-667-857-179
20	406	19.0	454	3	US-09-404-879A-180
21	406	19.0	454	4	US-09-338-933-180
22	406	19.0	454	4	US-09-215-681-180
23	406	19.0	454	4	US-09-216-003A-180
24	406	19.0	454	4	US-09-667-857-180
25	401	18.8	401	4	US-09-702-705-1034
26	401	18.8	401	4	US-09-736-457-1034
27	401	18.8	401	4	US-09-614-124B-1034



```

; APPLICANT: TERMINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
;
; ROBEY, PAMELA G.
;
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
;
; NUMBER OF SEQUENCES: 13
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/07/432,044
;
; FILING DATE: 03-NOV-1989
;
; SEQ ID NO:12:
;
; LENGTH: 933
;
5340934-12

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Query Match	43.5%	Score 928.2	DB 6	Length 933
Best Local Similarity	99.7%	Pred. No. 1.1e-236		
Matches 930	Conservative 0	Mismatches 3	Indels 0	Gaps 0

QY	37	CCACTGAGGGTTCCACGACCACCATGAGGGCCCTGGATCTTTCTTTCCTTTGCTGCTGCGCGGG	96
DB	1	CCACTAAGGGTTCCAGCAGCATGAGGGCCCTGGATCTTTCTTTCCTTTGCTGCTGCGCGGG	60
QY	97	AGGCCCTTGGCAGCCCTTCAGCAAGAAAGCCCTGCCTGATGAGACAGAGGTGGTGAAGAA	156
DB	61	AGGCCCTTGGCAGCCCTTCAGCAAGAAAGCCCTGCCTGATGAGACAGAGGTGGTGAAGAA	120
QY	157	ACTGTGCGAGGGTCACTGAGGTATCTGTGGAGCTAATCTGTTCAGAGTGGAGTAGGA	216
DB	121	ACTGTGCGAGGGTCACTGAGGTATCTGTGGAGCTAATCTGTTCAGAGTGGAGTAGGA	180
QY	217	GAATTTTGATGATGTGTGAGAGAAACCGAAGAGGAGTGTGGCGGAAATCCCTGCCAG	276
DB	181	GAATTTTGATGATGTGTGAGAGAAACCGAAGAGGAGTGTGGCGGAAATCCCTGCCAG	240
QY	277	AACCAACACTGCAAAACHCGGCAAGGTGTGCGAGCTGGATGAGAACAAACCCCATGTGC	336
DB	241	AACCAACACTGCAAAACHCGGCAAGGTGTGCGAGCTGGATGAGAACAAACCCCATGTGC	300
QY	337	GTGTGCCAGAGACCCACACAGCTGCCAGCCCCCAATGCGCAGTTTGAGAGGTGTGCAGC	396
DB	301	GTGTGCCAGAGACCCACACAGCTGCCAGCCCCCAATGCGCAGTTTGAGAGGTGTGCAGC	360
QY	397	AATGACAAACAGACCTTTCGACTCTTCTCGCCACTCTTTTGGCCACAAAGTGACCCCTGGAG	456
DB	361	AATGACAAACAGACCTTTCGACTCTTCTCGCCACTCTTTTGGCCACAAAGTGACCCCTGGAG	420
QY	457	GGCACCAGAAAGGGCCACAGCTCCACTGGACTACATCGGGCCTTGGAAATACATCCCC	516
DB	421	GGCACCAGAAAGGGCCACAGCTCCACTGGACTACATCGGGCCTTGGAAATACATCCCC	480
QY	517	CTTTGCTGGACTCTGAGCTGACCGAATTCCTCCCTGCGCATGCGGGACTGCTCAAGAAC	576
DB	481	CTTTGCTGGACTCTGAGCTGACCTGAATTCCTCCCTGCGCATGCGGGACTGCTCAAGAAC	540
QY	577	GTCTGTGTACCTTGATGAGGGATGAGGACAAACCTTTCTGACTGAGAAGCAGAAG	636
DB	541	GTCTGTGTACCTTGATGAGGGATGAGGACAAACCTTTCTGACTGAGAAGCAGAAG	600
QY	637	CTGGGGTGAAGATTCATGAAATGAGAGCGCTTGGGGCAGGAGACCCCGCTG	696
DB	601	CTGGGGTGAAGAAATTCATGAAATGAGAAAGCGCTTGGAGGAGGAGACCCCGCTG	660
QY	697	GAGCTGTGCGCCGGGACTTCGAGAGAACTATATAACATGTACATCTTCCCTGTACACTGG	756
DB	661	GAGCTGTGCGCCGGGACTTCGAGAGAACTATATAACATGTACATCTTCCCTGTACACTGG	720
QY	757	CAGTTGGCCAGCTGGACAGACCCCATTTGACGGGTACCTCTCCCAACCGAGCTGGCT	816
DB	721	CAGTTGGCCAGCTGGACAGACCCCATTTGACGGGTACCTCTCCCAACCGAGCTGGCT	780
QY	817	CCACTGGTGTCTCCCTCATCTCCCATGGACATTGCACCCCGCTTTTTCGAGACCTGT	876
DB	781	CCACTGGTGTCTCCCTCATCTCCCATGGAGCATTTGCACCCCGCTTTTTCGAGACCTGT	840
QY	877	GACCTGGAACAATGACAAAGTACATCGCCCTTGSATGAGTGGGCGGCTGCTTCGGCATCAAG	936

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Db      841  GACCTGCACATGACAAGTACATCGCCCTGGATGAGTGGCGGGCTGCTTCGGCATCAAG  900
Qy      937  CAGAAGGATATCGACAAGGATCTTTGTGATCTAA  969
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Db      901  CAGAAGGATATCGACAAGGATCTTTGTGATCTAA  933
      |||||
RESULT 3
5340934-12
; Patent No. 5340934
; APPLICANT: TERMEINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO:12:
; LENGTH: 933
5340934-12

```

	Query Match	43.5%	Score 928.2;	DB 6;	Length 933;
	Best Local Similarity	99.7%;	Pred.	No. 1.le-236;	
	Matches	930; Conservative	0;	Mismatches 3;	Indels 0;
Gaps					
Qy	37	CCACTGAGGGTTCCCACGACCATCAGCGGCCTTGATCTTCTTCCTCTGTGCCCTGCACCGG	96		
Dd	1	CCACTAAGGGTTCCAGCACCATGAGGCCCCGTGAATCTTCTCTCTTTCCTTGCCTGGCCGG	60		
Qy	97	AGGCGCTTTGGCAGCGCCCTCAGCAAGAAGCCCTGCCTGTATGAGACAGAGGTGTTGAAAGAA	156		
Dd	61	AGGCGCTTTGGCAGCGCCCTCAGCAAGAAGCCCTGCCTGTATGAGACAGAGGTGTTGAAAGAA	120		
Qy	157	ACTGTGCAGAGGTGACTGAGGTATCTGTGGAGGCTTAATCTCTGTCCAGGTGAAAGTAGGA	216		
Dd	121	ACTGTGCAGAGGTGACTGAGGTATCTGTGGAGCTATTCTGTCCAGGTGAAAGTAGGA	180		
Qy	217	GAATTTGATGATGTGTGAGAGGAACAACGAGAGAGGTGTGGCGGAAAAATCCCTGCCAG	276		
Dd	181	GAATTTGATGATGTGTGAGAGGAACAACGAGAGAGGTGTGGCGGAAAAATCCCTGCCAG	240		
Qy	277	AACCACCACTGCAAAACACGGCAAAGGTGTGCGAGCTGGAATGAGAACCAACCCCCATGTGC	336		
Dd	241	AACCACCACTGCAAAACACGGCAAAGGTGTGCGAGCTGGAATGAGAACCAACCCCCATGTGC	300		
Qy	337	GTGTGCCAGACCCCAACAGCTGCCAGCCCCCAATTGGCGAGTTTTGAGAAGGTGTGCAGC	396		
Dd	301	GTGTGCCAGACCCCAACAGCTGCCAGCCCCCAATTGGCGAGTTTTGAGAAGGTGTGCAGC	360		
Qy	397	AANTGACAAAGACCTTCGACTCTTCCTGCCACCTCTTCCTGCCACAAAGTGCAACCCCTGGAG	456		
Dd	361	AANTGACAAAGACCTTCGACTCTTCCTGCCACCTCTTCCTGCCACAAAGTGCAACCCCTGGAG	420		
Qy	457	GGCACCAAGAGGGSCCAAAAGCTCCAACCTGGACTACATCGGGCCCTTGCAAAATACATCCCC	516		
Dd	421	GGCACCAAGAGGGSCCAAAAGCTCCAACCTGGACTACATCGGGCCCTTGCAAAATACATCCCC	480		
Qy	517	CCTTGCCCTGGAAGGCTGACGAGTGAACGAATAATCCCCCTGGCGCATCGGGGACTGGCTCAAGAC	576		
Dd	481	CCTTGCCCTGGAAGGCTGACGAGTGAATAATCCCCCTGGCGCATCGGGGACTGGCTCAAGAAC	540		
Qy	577	GTCTGTGTCACCTGTATGAGAGGATGAGGACAAACACCTTCTGACTGAGAAGCAGAG	636		
Dd	541	GTCTGTGTCACCTGTATGAGAGGATGAGGACAAACACCTTCTGACTGAGAAGCAGAG	600		
Qy	.637	CTCGGGTGAAGAAGATCCATGAGAAATGAGAAGCGCCTGGAGGACAGGAGACCAACCCCFG	696		
Dd	601	CTCGGGTGAAGAAGATCCATGAGAAATGAGAAGCGCCTGGAGGACAGGAGACCAACCCCFG	660		
Qy	697	GAGCTGCTGCCCGGGACTTCGAGAGNAATATTAACATGTATCATCTTCCCTGTACACTGG	756		
Dd	661	GAGCTGCTGCCCGGGACTTCGAGAGNAATATTAACATGTATCATCTTCCCTGTACACTGG	720		



```

: APPLICANT: Tanaka, Hiroaki
: TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
: FILE REFERENCE: 91.US6.DIV
: CURRENT APPLICATION NUMBER: US/10/000,489
: CURRENT FILING DATE: 2001-11-14
: PRIOR APPLICATION NUMBER: US 09/924,340
: PRIOR FILING DATE: 2001-08-06
: PRIOR APPLICATION NUMBER: PCT/IB01/01715
: PRIOR FILING DATE: 2001-08-06
: PRIOR APPLICATION NUMBER: US 60/305,456
: PRIOR FILING DATE: 2001-07-13
: PRIOR APPLICATION NUMBER: US 60/302,277
: PRIOR FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: US 60/298,698
: PRIOR FILING DATE: 2001-06-15
: PRIOR APPLICATION NUMBER: US 60/293,574
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 112
: SOFTWARE: Jpatent
: SEQ ID NO 19
: LENGTH: 844
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: 1..111
: NAME/KEY: CDS
: LOCATION: 112..813
: NAME/KEY: 3'UTR
: LOCATION: 814..844
: US-10-000-489-19

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	Query Match	33.5%;	Score	713.6;	DB	4;	Length	844;		
	Best Local Similarity	99.4%;	Pred.	No. 1.4e-179;						
	Matches	716;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
Qy	1	CGGAGAGCGCCTCTGCCTGCCGCCCTGCCCTCCCTGCACATGAGGGTTCCACGACCAATG	60							
Dd	55	CCGGAGAGCGCCTCTGCCTGCCGCCCTGCCCTCCCTGCACATGAGGGTTCCACGACCAATG	114							
Qy	61	AGGECCTGGATCTTCTTTTCCTTTTGCTGTGCCCCGAGGGCCTTTGGCAGGCCCTTCAGCAA	120							
Dd	115	AGGECCTGGATCTTCTTTTCCTTTTGCTGTGCCCCGAGGGCCTTTGGCAGGCCCTTCAGCAA	174							
Qy	121	GAAGCCCTGCTGATGAGACAGAGGTGGTGGAAAGAACTGTGSCAGAGGTGACTGAGGTA	180							
Dd	175	GAAGCCCTGCTGATGAGACAGAGGTGGTGGAAAGAACTGTGSCAGAGGTGACTGAGGTA	234							
Qy	181	TCTGTGGGAGCTAATCCTGTGCCAGTGGAGTAGAGAAATTGATGATGGTGACAGAGAA	240							
Dd	235	TCTGTGGAGCTAATCCTGTGCCAGTGGAGTAGAGAAATTGATGATGGTGACAGAGAA	294							
Qy	241	ACCAGAGAGAGTGGTGGCGGAAAAATCCCTGCCAGAACCAACCACTGCATAACACGGCAAG	300							
Dd	295	ACCAGAGAGAGTGGTGGCGGAAAAATCCCTGCCAGAACCAACCACTGCATAACACGGCAAG	354							
Qy	301	GTGTGCCAGCTGGATGAGAACAACACCCCACATGTGCTGTGCCAGAGACCCACACAGCTGC	360							
Dd	355	GTGTGCCAGCTGGATGAGAACAACACCCCACATGTGCTGTGCCAGAGACCCACACAGCTGC	414							
Qy	361	CCAGCCCCCATTTGGCGAGTTTGAAGAGGTGTGCAGCAATGACAAACAAGACCTTCGACTCT	420							
Dd	415	CCAGCCCCCATTTGGCGAGTTTGAAGAGGTGTGCAGCAATGACAAACAAGACCTTCGACTCT	474							
Qy	421	TCTTGCCAATCTTTTGGCCAAGTGGCAACCTGTGAGGGGCAACCAAGAGGGGCCAACAGCTC	480							
Dd	475	TCTTGCCAATCTTTTGGCCAAGTGGCAACCTGTGAGGGGCAACCAAGAGGGGCCAACAGCTC	534							
Qy	481	CACCTGACTACATCGGGCCTTGCAATACATCCCCCTTTGCCCTGGACTCTGAGCTGACC	540							
Dd	535	CACCTGACTACATCGGGCCTTGCAATACATCCCCCTTTGCCCTGGACTCTGAGCTGACC	594							
Qy	541	GAATTTCCCTCGGCGATCGGGGACTGGCTCAAGAACCTCTCTGGTGCACCTGTATGAGAGG	600							

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595 GAATTCCTCCCTGCGCATGCGGGACTGGCTCAAGAACGCTCCTGGTCACCTCTGTATGAGAGG
601 GATGAGGACAAACACCTTCTTGACTGAGAAGCAGAGACTGCGGGTGAAGAAGATCCATGAG
655 GATGAGGACAAACACCTTCTTGACTGAGAAGCAGAGACTGCGGGTGAAGAAGATCCATGAG
661 AATGAGAAGCGCCTGGAGGCAAGGAGACCAACCCCGTGGAGAGCTGCTGCCCGCGGACTTCGAG
715 AATGAGAAGCGCCTGGAGGCAAGGAGACCAACCCCGTGGAGAGCTGCTGCCCGCGGACTGCCAG

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Query Match	22.0%	Score 469	DB 4	Length 481
Best Local Similarity	99.8%	Pred. No. 1.4e-114		
Matches 480	Conservative 0	Mismatches 0	Indels 1	Gaps 1
Qy	143	AGGTGGTGGAGAAACTGTGSCA-GAGGTGACTGAGGTATCTGTGGGAGCTAAATCTCTGTC	201	
Db	1	AGGTGGTGGAGAAAACTGTGGCAGAGGTGACTGAGGTATCTGTGGGAGCTAAATCTCTGTC	60	
Qy	202	CAGGTGGAAGTAGGAGAAATTGTATGTGTGCAGAGGAAACCGAAGAGGAGGTGTGTGGCG	261	
Db	61	CAGGTGGAAGTAGGAGAAATTGTATGTGTGCAGAGGAAACCGAAGAGGAGGTGTGTGGCG	120	
Qy	262	GAATAATCCCTGCCAGAACCACTCTGCNAACACGCGCAAGGTGTGCGAGCTGGATGAGAAC	321	
Db	121	GAATAATCCCTGCCAGAACCACTCTGCNAACACGCGCAAGGTGTGCGAGCTGGATGAGAAC	180	
Qy	322	AACACCCCCATGTGCGTGTGCCAGACCCCAACACAGCTGCCACGCCCCCAATTGGCCAGTTT	381	
Db	181	AACACCCCCATGTGCGTGTGCCAGACCCCAACACAGCTGCCACGCCCCCAATTGGCCAGTTT	240	
Qy	382	GAGAAGGTGTGCAGCAATGCAACAAGACCTTTGACTCTTCTGTGCACCTTCTTTTGCCACA	441	
Db	241	GAGAAGGTGTGCAGCAATGCAACAAGACCTTTGACTCTTCTGTGCACCTTCTTTTGCCACA	300	
Qy	442	AAGTGCAACCTTGAGGGGCAACAAGAGGGGCCACAAGCTCCACCTGGACTACATCGGGCCT	501	
Db	301	AAGTGCAACCTTGAGGGGCAACAAGAGGGGCCACAAGCTCCACCTGGACTACATCGGGCCT	360	
Qy	502	TGCNAATACATCCCCCTTCGCTGGACTCTGAGCTGACCGGAATTCGCCCTCGGCATGGCG	561	
Db	361	TGCNAATACATCCCCCTTCGCTGGACTCTGAGCTGACCGGAATTCGCCCTCGGCATGGCG	420	
Qy	562	GACTGGCTCAAGAACGTCTCGTGCACCTGTATGAGAGGGATGAGGACAACAACCTTCTG	621	
Db	421	GACTGGCTCAAGAACGTCTCGTGCACCTGTATGAGAGGGATGAGGACAACAACCTTCTG	480	
Qy	622	A 622		
Db	481	A 481		





Query Match	22.0%; Score 469; DB 4; Length 481;	
Best Local Similarity	99.8%; Pred. No. 1.4e-114;	
Matches 480; Conservative	0; Mismatches	1; Indels 1; Gaps 1;
QY	143	AGGTGCTGGAAGAACTGTGGCA-GAGGTGACTGAGGTATCTGTGGAGCTTAATCCCTGTC 201
DB	1	AGGTGCTGGAAGAACTGTGGCAAGAGTCTGAGGTATCTGTGGAGCTTAATCCCTGTC 60
QY	202	CAGGTGGAAGTAGGAAATTTGATGATGCTGAGAGGAAACCGAAGAGGAGGTGGTGGCG 261
DB	61	CAGGTGGAAGTAGGAAATTTGATGATGCTGAGAGGAAACCGAAGAGGAGGTGGTGGCG 120
QY	262	GAAATCCCTGCGAGAACCACTGCAACACGCGCAGAGGTGCGAGCTGGATGGAAC 321
DB	121	GAAATCCCTGCGAGAACCACTGCAACACGCGCAGAGGTGCGAGCTGGATGGAAC 180
QY	322	AACACCCCATGTGCGTGTGCCAGGACCCCACTGAGCTGCCAGCCCATTTGGCGAGTTT 381
DB	181	AACACCCCATGTGCGTGTGCCAGGACCCCACTGAGCTGCCAGCCCATTTGGCGAGTTT 240
QY	382	GAGAAGGTGTGAGCAATGACAACAGACCTTGCATCTTCTCGCACTTTTGGCCACA 441
DB	241	GAGAAGGTGTGAGCAATGACAACAGACCTTGCATCTTCTCGCACTTTTGGCCACA 300
QY	442	AGTGCACCTCTGAGGGCACCAAGAGGGCCACAAGCTCCACCTGGACTACATCGGSCCT 501
DB	301	AGTGCACCTCTGAGGGCACCAAGAGGGCCACAAGCTCCACCTGGACTACATCGGSCCT 360
QY	502	TGCAATATACATCCCCCTTGGCTGGAGCTCTGAGCTGACCGAATTTCCCTCGCGCATCGG 561
DB	361	TGCAATATACATCCCCCTTGGCTGGAGCTCTGAGCTGACCGAATTTCCCTCGCGCATCGG 420
QY	562	GACTGCTCAAGAACTCTGTGTCACCTGTATGAGAGGATGAGGACAACACTTCTG 621
DB	421	GACTGCTCAAGAACTCTGTGTCACCTGTATGAGAGGATGAGGACAACACTTCTG 480
QY	622	A 622
DB	481	A 481
RESULT 10		
US-09-640-173-189		
Sequence 189, Application US/09640173		
Patent No. 6613515		
GENERAL INFORMATION:		
APPLICANT: Xu, Jiangchun		
APPLICANT: Stolk, John A.		
TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND		
TITLE OF INVENTION: METHODS OF USE THEREFOR		
FILE REFERENCE: 210121.484C2		
CURRENT APPLICATION NUMBER: US/09/640,173		
CURRENT FILING DATE: 2000-08-15		
NUMBER OF SEQ ID NOS: 196		
SOFTWARE: FastSeq for Windows Version 3.0		
SEQ ID NO 189		
LENGTH: 460		
TYPE: DNA		
ORGANISM: Homo sapiens		
US-09-640-173-189		
Query Match	21.1%; Score 450.4; DB 4; Length 460;	
Best Local Similarity	98.7%; Pred. No. 1.2e-109;	
Matches 454; Conservative	0; Mismatches 6; Indels 0; Gaps 0;	
QY	1652	TTTTGGGAGCAGGACTGTGCAATTTCTCTGGGAAGTGTGTCAGCGCATCTCGAGGGCTTCT 1711
DB	1	TTTTGGGAGCAGGACTGTGCAATTTCTCTGGGAAGTGTGTCAGCGCATCTCGAGGGCTTCT 60
QY	1712	CCTCTCTGTCTTTTGGAGAACCAAGGCTCTTCTCAGGGGCTCTAGGGACTGCCAGGCTG 1771
DB	61	CCTCTCTGTCTTTTGGAGAACCAAGGCTCTTCTCAGGGGCTCTAGGGACTGCCAGGCTG 120
QY	1772	TTTCAGCCAGGAAGCCAAATCAAGAGTGAGATGTAGAAAGTTGTAAATATGAAGAAAGT 1831
DB	121	TTTCAGCCAGGAAGCCAAATCAAGAGTGAGATGTAGAAAGTTGTAAATATGAAGAAAGT 180
QY	1832	GGAGTTGTGTAATCGTTTGTCTTCTCCTCACATTTTGGATGATGTCATAGGTTTATGAG 1891
DB	181	GGAGTTGTGTAATCGTTTGTCTTCTCCTCACATTTTGGATGATGTCATAGGTTTATGAG 240
QY	1892	ATGTTCTCTCTTTTCTTCCCTCCCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1951
DB	241	ATGTTCTCTCTTTTCTTCCCTCCCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 300
QY	1952	GTTAATGGGATGCTCGGATCTCAGAGCTGAGAACTCGTTCACCTCAAGCAATTTTCATGA 2011
DB	301	GTTAATGGGATGCTCGGATCTCAGAGCTGAGAACTCGTTCACCTCAAGCAATTTTCATGA 360

Qy 2012 AAAAGCTGCTTCTTATTAAATCATACAAACTCTACCATGATGTGAAGAGTTTCAAAATC 2071  
Db 361 AAAAGCTGCTTCTTATTAAATCATACAAACTCTACCATGATGTGAAGAGTTTCAAAATC 420  
Qy 2072 TTTCAAAATAAAAGTAAATGACTTAGAACTGAAAAAAA 2111  
Db 421 CTTCAAAATAAAAGTAAATGACTTAGAACTGAAAAAAA 460

## RESULT 12

US-09-825-294-189  
; Sequence 189, Application US/09825294  
; Patent No. 6710170  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Stolk, John A.  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Fling, Steven P.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITL OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C5  
; CURRENT APPLICATION NUMBER: US/09/825,294  
; CURRENT FILING DATE: 2001-04-03  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 189  
; LENGTH: 460  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-825-294-189

Query Match 21.1%; Score 450.4; DB 4; Length 460;  
Best Local Similarity 98.7%; Pred. No. 1.2e-109;  
Matches 454; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1652 TTTTGGGAGCAGGACTGTCTGGAAGTGTCTGGAAGTGTCTGGAAGTGTCTGGAAGTGTCT 1711  
Db 1 TTTTGGGAGCAGGACTGTCTGGAAGTGTCTGGAAGTGTCTGGAAGTGTCTGGAAGTGTCT 60  
Qy 1712 CCTCCTCTGCTTTTGGAGAACCAAGGCTCTTCTCAGGGCTCTAGGACTGCCAGGCTG 1771  
Db 61 CCTCCTCTGCTTTTGGAGAACCAAGGCTCTTCTCAGGGCTCTAGGACTGCCAGGCTG 120  
Qy 1772 TTTCAAGCAGGAGCCAAATCAAGAGTGAGATGTAGAAAGTTGTAATAAGTAAAGT 1831  
Db 121 TTTCAAGCAGGAGCCAAATCAAGAGTGAGATGTAGAAAGTTGTAATAAGTAAAGT 180  
Qy 1832 GGAGTTGGTGAATCGGTGTTCTTCTCCTCAATTTGGATGATTTGTCATAGGTTTTCAGC 1891  
Db 181 GGAGTTGGTGAATCGGTGTTCTTCTCCTCAATTTGGATGATTTGTCATAGGTTTTCAGC 240  
Qy 1892 ATGTTCTCTCTTTTCTTCCACCTCCCTTTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1951  
Db 241 ATGTTCTCTCTTTTCTTCCACCTCCCTTTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 300  
Qy 1952 GTTAATGGAGTGTGGATCTCACAGGCTGAGAACTCGTTCCACCTCCAAAGCAATTCATGA 2011  
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Db 361 AAAAGCTGCTTCTTATTAAATCATACAAACTCTACCATGATGTGAAGAGTTTCAAAATC 420  
Qy 2072 TTTCAAAATAAAAGTAAATGACTTAGAACTGAAAAAAA 2111  
Db 421 CTTCAAAATAAAAGTAAATGACTTAGAACTGAAAAAAA 460

## RESULT 13

US-09-970-966-189  
; Sequence 189, Application US/09970966  
; Patent No. 6720146  
; GENERAL INFORMATION:

; APPLICANT: Stolk, John A.  
; APPLICANT: Molesh, David Alan  
; APPLICANT: Fling, Steven P.  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITL OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.484C6  
; CURRENT APPLICATION NUMBER: US/09/970,966  
; CURRENT FILING DATE: 2001-10-02  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 189  
; LENGTH: 460  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-970-966-189

Query Match 21.1%; Score 450.4; DB 4; Length 460;  
Best Local Similarity 98.7%; Pred. No. 1.2e-109;  
Matches 454; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1652 TTTTGGGAGCAGGACTGTCTGGAAGTGTCTGGAAGTGTCTGGAAGTGTCTGGAAGTGTCT 1711  
Db 1 TTTTGGGAGCAGGACTGTCTGGAAGTGTCTGGAAGTGTCTGGAAGTGTCTGGAAGTGTCT 60  
Qy 1712 CCTCCTCTGCTTTTGGAGAACCAAGGCTCTTCTCAGGGCTCTAGGACTGCCAGGCTG 1771  
Db 61 CCTCCTCTGCTTTTGGAGAACCAAGGCTCTTCTCAGGGCTCTAGGACTGCCAGGCTG 120  
Qy 1772 TTTCAAGCAGGAGCCAAATCAAGAGTGAGATGTAGAAAGTTGTAATAAGTAAAGT 1831  
Db 121 TTTCAAGCAGGAGCCAAATCAAGAGTGAGATGTAGAAAGTTGTAATAAGTAAAGT 180  
Qy 1832 GGAGTTGGTGAATCGGTGTTCTTCTCCTCAATTTGGATGATTTGTCATAGGTTTTCAGC 1891  
Db 181 GGAGTTGGTGAATCGGTGTTCTTCTCCTCAATTTGGATGATTTGTCATAGGTTTTCAGC 240  
Qy 1892 ATGTTCTCTCTTTTCTTCCACCTCCCTTTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1951  
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Qy 1952 GTTAATGGAGTGTGGATCTCACAGGCTGAGAACTCGTTCCACCTCCAAAGCAATTCATGA 2011  
Db 301 GTTAATGGAGTGTGGATCTCACAGGCTGAGAACTCGTTCCACCTCCAAAGCAATTCATGA 360  
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Db 361 AAAAGCTGCTTCTTATTAAATCATACAAACTCTACCATGATGTGAAGAGTTTCAAAATC 420  
Qy 2072 TTTCAAAATAAAAGTAAATGACTTAGAACTGAAAAAAA 2111  
Db 421 CTTCAAAATAAAAGTAAATGACTTAGAACTGAAAAAAA 460

## RESULT 14

US-09-513-999C-141  
; Sequence 141, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 141  
; LENGTH: 490



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 17:10:02 ; Search time 1070 Seconds  
(without alignments)  
11800.755 Million cell updates/sec

Title: US-09-340-595A-1  
Perfect score: 2133  
Sequence: 1 cggagagcgcgtctgcct.....aaaaaaaaaaaaaaaaaaaaa 2133

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
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12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2133	100.0	2133	5	Aah76473
2	2133	100.0	2133	6	ABL62654
3	2133	100.0	2133	6	ABQ60778
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9	2133	100.0	2133	10	ADP81423
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13	2133	100.0	2133	12	ADP21420
14	2133	100.0	2133	12	ADQ25959
15	2133	100.0	2133	13	ADR25011
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21	2094.6	98.2	2101	13	ACN38288
22	2078	97.4	2128	4	Aah23081
23	2001.4	93.8	5347	10	ADB63156
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25	1819.4	85.3	3490	8	ACC46556
26	1818.8	85.3	3560	12	ADQ32225
27	1795.4	84.2	3815	5	ADL63443
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29	1426.8	66.9	2096	11	ACN89890
30	1344.2	63.0	2136	11	ACN92757
31	1304	61.1	1516	2	AAZ41955
32	1299.2	60.9	1344	10	ADI60505
33	1156.6	54.2	14769	4	AAI04404
34	1152.8	54.0	1691	4	Aah72501
35	1142.6	53.6	3747	12	ADQ65013
36	1024	48.0	1024	10	ABZ83860
37	1000.2	46.9	2079	2	AAV36502
38	1000.2	46.9	2079	6	AB199220
39	1000.2	46.9	2079	13	ADQ80835
40	990.6	46.4	3815	5	ADL63443
41	941.2	44.1	957	3	AAQ59231
42	928.2	43.5	933	2	AAQ04495
43	915.2	42.9	2025	6	ABK63650
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45	915.2	42.9	2025	10	ADB52558

ALIGNMENTS

RESULT 1

AAH76473  
ID AAH76473 standard; cDNA; 2133 BP.

AC AAH76473;

DT 22-OCT-2001 (first entry)

DE cDNA corresponding to human IFN-alpha induced gene encoding SPARC.  
KW Human; interferon-alpha induced gene; type I interferon treatment;  
KW chronic viral hepatitis; relapsing remitting multiple sclerosis;  
KW neoplastic disease; SPARC; IFN-alpha; interferon-alpha; ss.

OS Homo sapiens.

FH Key Location/Qualifiers  
CDS 58..969

FT FT /\*tag= a

FT FT /product= "SPARC"

XX WO200159155-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-GB000578.

XX PR 11-FEB-2000; 2000GB-00003203.

PR 11-FEB-2000; 2000GB-00003204.

PR 11-FEB-2000; 2000GB-00003205.

PR 11-FEB-2000; 2000GB-00003206.

PR 11-FEB-2000; 2000GB-00003207.

PR 11-FEB-2000; 2000GB-00003208.

PR 11-FEB-2000; 2000GB-00003210.

PR 11-FEB-2000; 2000GB-00003212.

PR 11-FEB-2000; 2000GB-00003213.

PR 11-FEB-2000; 2000GB-00003215.

PR 11-FEB-2000; 2000GB-00003216.

PR 11-FEB-2000; 2000GB-00003219.

PR 11-FEB-2000; 2000GB-00003220.

PR 11-FEB-2000; 2000GB-00003221.

PR 11-FEB-2000; 2000GB-00003222.

PR 17-FEB-2000; 2000GB-00003768.



OS	Homo sapiens.	
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XX	WO200194629-A2.	
PN		
XX		
XX	13-DEC-2001.	
XX		
XX	30-MAY-2001; 2001WO-US010838.	
XX		
PR	05-JUN-2000; 2000US-0209473P.	
PR	05-JUN-2000; 2000US-0209531P.	
PR	18-SEP-2000; 2000US-0233133P.	
PR	18-SEP-2000; 2000US-0233617P.	
PR	20-SEP-2000; 2000US-0234009P.	
PR	20-SEP-2000; 2000US-0234034P.	
PR	20-SEP-2000; 2000US-0234052P.	
PR	22-SEP-2000; 2000US-0234509P.	
PR	22-SEP-2000; 2000US-0234567P.	
PR	25-SEP-2000; 2000US-0234923P.	
PR	25-SEP-2000; 2000US-0234924P.	
PR	25-SEP-2000; 2000US-0235077P.	
PR	25-SEP-2000; 2000US-0235082P.	
PR	25-SEP-2000; 2000US-0235134P.	
PR	25-SEP-2000; 2000US-0235280P.	
PR	26-SEP-2000; 2000US-0235637P.	
PR	26-SEP-2000; 2000US-0235638P.	
PR	27-SEP-2000; 2000US-0235711P.	
PR	27-SEP-2000; 2000US-0235720P.	

	Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
XX	Claim 1; SEQ ID NO 991; 44pp; English.
XX	The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms tumour
XX	
SQ	Sequence 2133 BP; 543 A; 533 C; 521 G; 536 T; 0 U; 0 Other;
	Query Match            100.0%; Score 2133; DB 6; Length 2133;
	Best Local Similarity    100.0%; Pred. No. 0;
	Matches 2133; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
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DB	1 CGGGAGAGCGCCTTCGCTGCCTGCCCTGCTGCTGCCACTGAGGGTTCCACGACCATG 60
QY	'61 AGGGCTTGATCTTCTTCTCTTTGCTGGCGGAGGGCCCTTGGCAGGCCCTCAGCAA 120
DB	61 AGGGCTTGATCTTCTTCTCTTTGCTGGCGGAGGGCCCTTGGCAGGCCCTCAGCAA 120
QY	121 GAAGCCCTGCCGTGATGAGACAGAGGTGGTGGGAAGAACTGTGGCAGAGGTGACTGAGGTA 180
DB	121 GAAGCCCTGCCGTGATGAGACAGAGGTGGTGGGAAGAACTGTGGCAGAGGTGACTGAGGTA 180

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Db 181 TCTGTGGAGCTAATCTCTCCAGGTGGAGTGGAGAAATTTGATGATGGTGAGAGAA 240
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QY 1861 ACATTTGGATGTATGTCATTAAGGTTTTCAGATGTTTCTCTCTTTTTCACCCCTCCCTTT 1920
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QY 1921 TGTCTTCTTATTAATCAAGAGAACTTCAAGTTAAATGGGATGTCGGGATCTCACAGGCT 1980
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QY 1981 GAGAACTCGTTCCACTCCAAAGCATTTTCATGAAAAAGCTGCTTCTTATTAATCATACAAAC 2040
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## RESULT 3

ABQ60778  
ID ABQ60778 standard; cDNA; 2133 BP.

XX ABQ60778;

AC AC

XX AC

DT 02-AUG-2002 (first entry)

XX Human SPARC/Osteonectin cDNA sequence SEQ ID NO:4476.

XX Human; colon cancer; cancer; tissue profiling; forensic; mapping;

KW genetic analysis; diagnostic; antisense therapy; gene; ss.

XX







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1861 ACATTTGAGATGATGTCATAGAGTTTGTAGCATGTTTCTCTCTCTCTCTCTCTCTCT 1920  
1921 TGTCTCTCTATTAATCAAGAGAACTTCAAAAGTGAATGGAGTGGTGGATCTCACAGGCT 1980  
1921 TGTCTCTCTATTAATCAAGAGAACTTCAAAAGTGAATGGAGTGGTGGATCTCACAGGCT 1980  
1981 GAGAACTCGTTCACCTCCAAGCATTTTCATGAAAAAGCTGCTTCTTATTAATCATACAAAC 2040  
1981 GAGAACTCGTTCACCTCCAAGCATTTTCATGAAAAAGCTGCTTCTTATTAATCATACAAAC 2040  
2041 TCTCACCATGATGTGAAGTTTCAAACTTTTCAAAATAAAAGTAAATGATCTTAGAAA 2100  
2041 TCTCACCATGATGTGAAGTTTCAAACTTTTCAAAATAAAAGTAAATGATCTTAGAAA 2100  
2101 CTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2133  
2101 CTGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2133

## RESULT 5

ABN95593

ID ABN95593 standard; DNA; 2133 BP.

XX AC ABN95593;

XX DT 13-AUG-2002 (first entry)

XX DE Gene #2091 used to diagnose liver cancer.

XX KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;  
metastatic liver tumour; cytostatic; expression profile; disease state;  
disease progression; drug toxicity; drug efficacy; drug metabolism.

XX OS Homo sapiens.

XX PN WO200229103-A2.

XX PD 11-APR-2002.

XX PF 02-OCT-2001; 2001WO-US030589.

XX PR 02-OCT-2000; 2000US-0237054P.

XX (GENE-) GENE LOGIC INC.

XX PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

XX WPI; 2002-426119/45.

XX PT Diagnosing and detecting the progression of liver cancer, hepatocellular  
carcinoma or metastatic liver tumor in a patient, involves detecting the  
level of expression of two or more genes in a liver tissue sample.

XX PS Claim 1; SEQ ID NO 2091; 298pp; English.





961 GTGATCTAAATCCACTCTCTCCACAGTACCGGATTCTCTCTTTAAACCCCTCCCTTCGTGT 1020  
Db GTGATCTAAATCCACTCTCTCCACAGTACCGGATTCTCTCTTTAAACCCCTCCCTTCGTGT 1020  
Qy TTCCCCCAATGTTTAAATGTTTCGATGTTTGGTGTCTGCGCTGGAGACAAGGTGCTAA 1080  
Db TTCCCCCAATGTTTAAATGTTTCGATGTTTGGTGTCTGCGCTGGAGACAAGGTGCTAA 1080  
Qy CATAGATTTAAGTGAATACATTAACGGTGTCTAAATAATGAAATCTTAACCCCAAGACATGA 1140  
Db CATAGATTTAAGTGAATACATTAACGGTGTCTAAATAATGAAATCTTAACCCCAAGACATGA 1140  
Qy CATCTTACGTGTAACTTAACCTTAAGAGCCCTTTTCCACAGCGATTAATAGTCCCATTTT 1200  
Db CATCTTACGTGTAACTTAACCTTAAGAGCCCTTTTCCACAGCGATTAATAGTCCCATTTT 1200  
Qy TCTCTGCGCATTTGTAGCTTTGGCCATTTGCTTATTTGGCAGATGGGTGGACCGGATCTG 1260  
Db TCTCTGCGCATTTGTAGCTTTGGCCATTTGCTTATTTGGCAGATGGGTGGACCGGATCTG 1260  
Qy CTGGGCTCTGCTTTAAACACACATTCGAGCTTCAACTTTTCTTTAGTGTCTCTGTTTGA 1320  
Db CTGGGCTCTGCTTTAAACACACATTCGAGCTTCAACTTTTCTTTAGTGTCTCTGTTTGA 1320  
Qy AACTAATACCTTACCAGTACAGACTTGTGTTCATTTCAATTCAGGGTCTTGGCTGCCTGT 1380  
Db AACTAATACCTTACCAGTACAGACTTGTGTTCATTTCAATTCAGGGTCTTGGCTGCCTGT 1380  
Qy GGGCTTCCCGAGTGGCTGGAGTGGGCAAGGAGTAACAGACACACAGATCTGTCA 1440  
Db GGGCTTCCCGAGTGGCTGGAGTGGGCAAGGAGTAACAGACACACAGATCTGTCA 1440  
Qy AGGATGTTTTGGGACTAGAGGCTCAGTGTGGGAGAGATCCCTGCAGAAATCCACCAACC 1500  
Db AGGATGTTTTGGGACTAGAGGCTCAGTGTGGGAGAGATCCCTGCAGAAATCCACCAACC 1500  
Qy AGAAGTGGTTTTGCTGAGGCTGTAACTGAGAGAAAGATTCCTGGGCTGTCTTATGAATA 1560  
Db AGAAGTGGTTTTGCTGAGGCTGTAACTGAGAGAAAGATTCCTGGGCTGTCTTATGAATA 1560  
Qy TATAGACATTTCTACATAAGCCAGTTCATCACATTTCTCTCTTTACCTTTTCAGTGCAG 1620  
Db TATAGACATTTCTACATAAGCCAGTTCATCACATTTCTCTCTTTACCTTTTCAGTGCAG 1620  
Qy TTTCTTTTTCATTTAGGCTGTGTCTAAACTTTTGGAGACACCGGACTGTCTGTCTG 1680  
Db TTTCTTTTTCATTTAGGCTGTGTCTAAACTTTTGGAGACACCGGACTGTCTGTCTGTG 1680  
Qy GGAAGTGTTCAGCGATCTCTGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740  
Db GGAAGTGTTCAGCGATCTCTGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740  
Qy CTTCTCAGGGGCTCTAGGAGCTGCGAGGCTGTTTTCAGCCAGAGGCGCAAAATCAAGAGT 1800  
Db CTTCTCAGGGGCTCTAGGAGCTGCGAGGCTGTTTTCAGCCAGAGGCGCAAAATCAAGAGT 1800  
Qy GAGATGTAGAAAGTTGTAAATAAGAAAGTGGAGTGGTGAATCGGTGTCTTTCTCTC 1860  
Db GAGATGTAGAAAGTTGTAAATAAGAAAGTGGAGTGGTGAATCGGTGTCTTTCTCTC 1860  
Qy ACATTTGGATGTCATAGGTTTTTGTAGCATGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920  
Db ACATTTGGATGTCATAGGTTTTTGTAGCATGTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920  
Qy TGTCTCTCTAATTAATCAAGAGAACTTCAAAAGTTAATGGAGTGTGCGGATCTCACAGGCT 1980  
Db TGTCTCTCTAATTAATCAAGAGAACTTCAAAAGTTAATGGAGTGTGCGGATCTCACAGGCT 1980  
Qy GAGAACTCGTTTCACTCCAGCATTTTCATGAAAAAGTGTCTTTTATTAATCATCAAAAC 2040  
Db GAGAACTCGTTTCACTCCAGCATTTTCATGAAAAAGTGTCTTTTATTAATCATCAAAAC 2040

Qy 2041 TCTCACCATGATGTGAGAGCTTTTCACAAATCTTTCAAAATATAAAAGTAATGACTTAGAAA 2100  
Db 2041 TCTCACCATGATGTGAGAGCTTTTCACAAATCTTTTCACAAATATAAAAGTAATGACTTAGAAA 2100  
Qy 2101 CTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133  
Db 2101 CTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2133

RESULT 7  
AAD48129  
ID AAD48129 standard; DNA; 2133 BP.  
XX AAD48129;  
XX DT 24-FEB-2003 (first entry)  
XX Human SPARC (osteonectin) DNA.  
XX Brain; tumour protein target; Tbt; ischaemic stroke; cancer; epilepsy;  
KW schizophrenia; depression; Alzheimer's disease; Parkinson's disease;  
KW Huntington's chorea; traumatic head injury; dementia; stupor; headache;  
KW coma; vertigo; weakness; myasthenia gravis; cerebrovascular disorder;  
KW infection; multiple sclerosis; pregnancy; medical illness; vasotropic;  
KW metabolic deficiency; cerebroprotective; antidepressant; antibacterial;  
KW cytosolic; nontropic; analgesic; fungicide; virucide; human; SPARC;  
XX osteonectin; gene; ds.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 58..969  
XX FT /\*tag= a  
XX FT /product= "Human SPARC (osteonectin) protein"  
XX WO200276510-A1.  
XX 03-OCT-2002.  
XX 22-MAR-2002; 2002WO-US008992.  
XX 23-MAR-2001; 2001US-00816703.  
XX 17-OCT-2001; 2001US-00983000.  
XX (AGYT-) AGY THERAPEUTICS INC.  
XX Mueller S, Melcher T, Chin DJ;  
XX WPI: 2003-029903/02.  
XX P-PSDB; AAE30336.  
XX Developing active agents that modulate the activity of a brain tumor  
XX protein target gene or gene product for treating e.g. stroke or cancer,  
XX comprises contacting an agent with a brain tumor protein.  
XX Claim 1; Page 100-103; 135pp; English.  
XX The invention relates to a method for developing biologically active  
XX agents that modulate activity of a brain tumour protein target (Tbt) gene  
XX or gene product. The method is useful for developing biologically active  
XX agents that modulate the activity of a brain tumour protein target gene  
XX or gene product. Compounds that bind to the brain tumour proteins are  
XX useful for treating e.g. ischaemic stroke, brain cancer, epilepsy,  
XX schizophrenia, depression, Alzheimer's disease, Parkinson's disease,  
XX Huntington's chorea, traumatic head injury, dementia, stupor, headache,  
XX coma, vertigo, weakness, myasthenia gravis, cerebrovascular disorders,  
XX infectious disorders (including fungal, bacterial, viral and parasitic  
XX infections), multiple sclerosis, and other complications associated with  
XX pregnancy, medical illness, alcohol and substance abuse, toxins and  
XX metabolic deficiencies. The brain tumour proteins may also be used to  
XX raise antibodies. The present sequence is human SPARC (osteonectin) DNA  
XX used to illustrate the method of the invention











Db 481 |CACCTGACATCATCGGGCTTGCATAATACATCCCCCTTGGCTGGACTGTGAGTCAAC 540  
Qy 541 |GAATTCCTCCCTGCGCATCGGGACTGGCTCAAGAACGTCTCTGGTCACTCTGATGAGAG 600  
Db 541 |GAATTCCTCCCTGCGCATCGGGACTGGCTCAAGAACGTCTCTGGTCACTCTGATGAGAG 600  
Qy 601 |GATGAGACAAACACCTTCTGACTGAGAGAGAGCTGGGGTGAAGAAGATCCATGAG 660  
Db 601 |GATGAGACAAACACCTTCTGACTGAGAGAGAGCTGGGGTGAAGAAGATCCATGAG 660  
Qy 661 |AATGAGAGCGCTGGAGGAGAGACACCCCTGGAGCTGTGGCCCGGGACTTCGAG 720  
Db 661 |AATGAGAGCGCTGGAGGAGAGACACCCCTGGAGCTGTGGCCCGGGACTTCGAG 720  
Qy 721 |AAGAACTATAACATGTATACATCTTCCCTGTACATCTGGCAGTTCCGCCACGACGAC 780  
Db 721 |AAGAACTATAACATGTATACATCTTCCCTGTACATCTGGCAGTTCCGCCACGACGAC 780  
Qy 781 |CCATGAGCGGTACCTCTCCCAACCGAGTGGCTCCACTGGTGCTCCCTCATCCCC 840  
Db 781 |CCATGAGCGGTACCTCTCCCAACCGAGTGGCTCCACTGGTGCTCCCTCATCCCC 840  
Qy 841 |ATGAGCATTTGCACACCCGCTTTTCGAGACCTGTGACCTGGACATGACAAGTACATC 900  
Db 841 |ATGAGCATTTGCACACCCGCTTTTCGAGACCTGTGACCTGGACATGACAAGTACATC 900  
Qy 901 |GCCCTGATGAGTGGGCGGCTGCTCCGCATCAAGCAGAGAGATATCGACAAGGATCTT 960  
Db 901 |GCCCTGATGAGTGGGCGGCTGCTCCGCATCAAGCAGAGAGATATCGACAAGGATCTT 960  
Qy 961 |GTGATCTAAATCCACTCTTCCACAGTACCGGATCTCTCTTTAACTCCCTCCCTGGT 1020  
Db 961 |GTGATCTAAATCCACTCTTCCACAGTACCGGATCTCTCTTTAACTCCCTCCCTGGT 1020  
Qy 1021 |TTCCCTCAATGTTTAAATGTTTGGATGTTGTTGTTCTGCTGGAGACAGGTGCTAA 1080  
Db 1021 |TTCCCTCAATGTTTAAATGTTTGGATGTTGTTGTTCTGCTGGAGACAGGTGCTAA 1080  
Qy 1081 |CATAGATTTAAGTGAATACATTAACCGTGTCTAAATAATGAATAATCTAACCAAGACATGA 1140  
Db 1081 |CATAGATTTAAGTGAATACATTAACCGTGTCTAAATAATGAATAATCTAACCAAGACATGA 1140  
Qy 1141 |CATCTTTAGCTGTAACCTTAATTAAGGCTTTTCCACAGCATTAATAGTCCCATTTT 1200  
Db 1141 |CATCTTTAGCTGTAACCTTAATTAAGGCTTTTCCACAGCATTAATAGTCCCATTTT 1200  
Qy 1201 |TCTCTGCCATTTGCTAGCTTGGCCATTTGCTTATGGCACATGGTGGACACGGATCTG 1260  
Db 1201 |TCTCTGCCATTTGCTAGCTTGGCCATTTGCTTATGGCACATGGTGGACACGGATCTG 1260  
Qy 1261 |CTGGGCTCTGCTTAAACACACATTCGAGCTTCAACTTTTCTTTAGTGTCTCTGTTGA 1320  
Db 1261 |CTGGGCTCTGCTTAAACACACATTCGAGCTTCAACTTTTCTTTAGTGTCTCTGTTGA 1320  
Qy 1321 |AATTAATCTTACCGAGTCAGACTTTGTTGTTTCAATTTCAATTCAGGGTCTGGCTGCT 1380  
Db 1321 |AATTAATCTTACCGAGTCAGACTTTGTTGTTTCAATTTCAATTCAGGGTCTGGCTGCT 1380  
Qy 1381 |GGGCTTCCCGAGTGGCTGGAGTGGGCAAGGAAAGTAAACACACACATGTTCTCA 1440  
Db 1381 |GGGCTTCCCGAGTGGCTGGAGTGGGCAAGGAAAGTAAACACACACATGTTCTCA 1440  
Qy 1441 |AGGATGTTTTGGGACTAGAGGCTCAGTGGTGGGAGAGATCCCTGCAGAAATCCCAACC 1500  
Db 1441 |AGGATGTTTTGGGACTAGAGGCTCAGTGGTGGGAGAGATCCCTGCAGAAATCCCAACC 1500  
Qy 1501 |AGACGTGTTTTGCTGAGGCTGTAACGAGAGAAAGTCTGGGGTGTCTTATGAAA 1560  
Db 1501 |AGACGTGTTTTGCTGAGGCTGTAACGAGAGAAAGTCTGGGGTGTCTTATGAAA 1560  
Qy 1561 |TATAGACATTTCTACATAAGCCAGTTTCATCACCATTTCTCTCTTACCTTTTCACTGTCAG 1620

Db 1561 |TATAGACATTTCTCACATAAGCCAGTTTCATCACCATTTCTCTCTTACCTTTCACTGTCAG 1620  
Qy 1621 |TTTCTTTTTCATATAGGCTGTGGTTCAAACCTTTTGGAGCACGAGTGTCTGTTCTCTG 1680  
Db 1621 |TTTCTTTTTCATATAGGCTGTGGTTCAAACCTTTTGGAGCACGAGTGTCTGTTCTCTG 1680  
Qy 1681 |GGAAGTGGTTCAGCGCATCTGCGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740  
Db 1681 |GGAAGTGGTTCAGCGCATCTGCGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740  
Qy 1741 |CTTCTCAGGGGCTCTAGGGACTGCGAGGCTGTTTTCAGCCAGGAGGCCAAAATCAAGAGT 1800  
Db 1741 |CTTCTCAGGGGCTCTAGGGACTGCGAGGCTGTTTTCAGCCAGGAGGCCAAAATCAAGAGT 1800  
Qy 1801 |GAGATGTAGAAAGTGTGAAATAGAAAAAGTGAGTGGTGAATCGGTTGTTCTTCTCTC 1860  
Db 1801 |GAGATGTAGAAAGTGTGAAATAGAAAAAGTGAGTGGTGAATCGGTTGTTCTTCTCTC 1860  
Qy 1861 |ACATTTGGATGATGTGTAAGGTTTTCAGCATGTTCTCTCTCTCTCTCTCTCTCTCTCT 1920  
Db 1861 |ACATTTGGATGATGTGTAAGGTTTTCAGCATGTTCTCTCTCTCTCTCTCTCTCTCTCT 1920  
Qy 1921 |TGTCTCTTATTAATCAAGAGAACTTCAAAGTTTAATGGATGTTGGATGTTCTTCTCTC 1980  
Db 1921 |TGTCTCTTATTAATCAAGAGAACTTCAAAGTTTAATGGATGTTGGATGTTCTTCTCTC 1980  
Qy 1981 |GAGAACTCGTTCACCTCCAGAGCATTTTCATGAAAAGCTGCTTCTTATTAATCATCAAA 2040  
Db 1981 |GAGAACTCGTTCACCTCCAGAGCATTTTCATGAAAAGCTGCTTCTTATTAATCATCAAA 2040  
Qy 2041 |TCTCACCATGATGTAAGAGTTCACAAATCTTTCAAATAAATAAGTAATGACTTGA 2100  
Db 2041 |TCTCACCATGATGTAAGAGTTCACAAATCTTTCAAATAAATAAGTAATGACTTGA 2100  
Qy 2101 |CTGAAAAA 2133  
Db 2101 |CTGAAAAA 2133

## RESULT 10

ADH2881  
ID ADH2881 standard; DNA; 2133 BP.  
XX  
AC ADH2881;  
XX  
XX 11-MAR-2004 (first entry)  
XX  
DE Human chronic myelogenous leukaemia (CML) gene marker #149.  
XX  
KW ds; chronic phase chronic myelogenous leukaemia; CP-CML;  
KW blast crisis CML; BC-CML; human; chronic myelogenous leukaemia;  
KW gene marker.  
XX  
OS Homo sapiens.  
XX  
XX US2003104426-A1.  
XX  
XX 05-JUN-2003.  
XX  
XX 14-JUN-2002; 2002US-00171581.  
XX  
XX 18-JUN-2001; 2001US-0298914P.  
XX  
PA (LINSLEY) LINSLEY P S.  
PA (MAOM) MAO M.  
PA (DAIH) DAI H.  
PA (HEY) HE Y.  
PA (RADJ) RADICH J P.  
XX  
XX Linsley PS, Mao M, Dai H, He Y, Radich JP;  
XX WPI; 2003-787046/74.  
XX

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QY 1921 TGTTCCTCTATTATCAAGAGAACTTCAAGTTAATGGGATGTCGGATCTCACAGGCT 1980
Db 1921 TGTTCCTCTATTATCAAGAGAACTTCAAGTTAATGGGATGTCGGATCTCACAGGCT 1980
QY 1981 GAGAACTCGTTCACCTCCAAGCATTTTCATGAAAAGCTGCTTCTTATTATATCATACAAC 2040
Db 1981 GAGAACTCGTTCACCTCCAAGCATTTTCATGAAAAGCTGCTTCTTATTATATCATACAAC 2040
QY 2041 TCTCACCATGATGTAAGAGTTTCAAAATCTTTCAAAATATAAAAGTAATGACTTAGAAA 2100
Db 2041 TCTCACCATGATGTAAGAGTTTCAAAATCTTTCAAAATATAAAAGTAATGACTTAGAAA 2100
QY 2101 CTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA 2133
Db 2101 CTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA 2133

RESULT 11
ADL35831
ID ADL35831 standard; DNA; 2133 BP.
XX
AC ADL35831;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human SPARC (secreted protein, acidic, cysteine-rich; osteonectin) DNA.
XX
KW angiogenesis; cytostatic; cancer; gene therapy; human; ds; SPARC;
KW secreted protein, acidic, cysteine-rich; osteonectin; gene.
XX
OS Homo sapiens.
XX
PN WO2004019893-A2.
XX
PD 11-MAR-2004.
XX
PF 02-SEP-2003; 2003WO-US027523.
XX
PR 30-AUG-2002; 2002US-00231956.
XX
PA (RIGE-) RIGEL PHARM INC.
XX
PI Lorens JB, Bogenberger J, Holland S, Xu W;
XX
DR WPI; 2004-239116/22.
DR P-PSDB; ADL35832.
XX
PT Identifying a compound that modulates angiogenesis for treating e.g.,
PT cancer comprises contacting the compound with a nucleic acid or
PT polypeptide and determining the functional effect of the compound upon
PT the nucleic acid or polypeptide.
XX
PS Claim 1; SEQ ID NO 439; 245pp; English.
XX
CC The invention relates to a novel method for identifying a compound that
CC modulates angiogenesis which comprises contacting the compound with a
CC nucleic acid, or a polypeptide encoded by a nucleic acid, that hybridises
CC under stringent conditions to a second nucleic acid and determining the
CC functional effect of the compound upon the nucleic acid or polypeptide.
CC The method of the invention has cytostatic applications and may be useful
CC for identifying a compound that modulates angiogenesis for treating
CC cancer or for use during gene therapy procedures. The current sequence is
CC that of an angiogenesis-related human DNA of the invention.
XX
SQ Sequence 2133 BP; 543 A; 533 C; 521 G; 536 T; 0 U; 0 Other;

Query Match 100.0%; Score 2133; DB 12; Length 2133;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGAGAGCGCGCTCTGCCTGCGCGCTGCTGCCACTGAGGGTTCACGACCATG 60
Db 61 AGGCGCTGGATCTTCTTTTCTCTTTTGCCTGGCGGAGGCCCTTGGCAGCCCTCAGCAA 120
Db 61 AGGCGCTGGATCTTCTTTTCTCTTTTGCCTGGCGGAGGCCCTTGGCAGCCCTCAGCAA 120
QY 121 GAAGCCCTGCTGATGAGACAGAGGTGGTGGAGAACTGTGCAGAGGTGACTGAGGTA 180
Db 121 GAAGCCCTGCTGATGAGACAGAGGTGGTGGAGAACTGTGCAGAGGTGACTGAGGTA 180
QY 181 TCTGTGGAGCTAATCTGTCCAGGTGGAAGTAGGAGAAATTTGATGATGTGTCAGAGGAA 240
Db 181 TCTGTGGAGCTAATCTGTCCAGGTGGAAGTAGGAGAAATTTGATGATGTGTCAGAGGAA 240
QY 241 ACCGAGAGAGAGGTGGTGGCGGAAAATCTCTGCAGAAACCACTGCAACACCGGCAAG 300
Db 241 ACCGAGAGAGAGGTGGTGGCGGAAAATCTCTGCAGAAACCACTGCAACACCGGCAAG 300
QY 301 GTGTGGAGCTGGATGAGAACACACCCCATGTGCTGCTGCCAGGACCCACAGCTGC 360
Db 301 GTGTGGAGCTGGATGAGAACACACCCCATGTGCTGCTGCCAGGACCCACAGCTGC 360
QY 361 CCAGCCCCCATTTGGCGAGTTTGAAGGTGTGCAGCAATGACAAACAGACTTCGACTCT 420
Db 361 CCAGCCCCCATTTGGCGAGTTTGAAGGTGTGCAGCAATGACAAACAGACTTCGACTCT 420
QY 421 TCTGTGCATCTTTTGGCAAAAGTGACCTGTGAGGGGCAACCAAGAGGGGCAACAGCTC 480
Db 421 TCTGTGCATCTTTTGGCAAAAGTGACCTGTGAGGGGCAACCAAGAGGGGCAACAGCTC 480
QY 481 CACTGTGACTACATCGGGGCTTGCAAATACATCCCCCTTGCCTGGACTCTGAGCTGACC 540
Db 481 CACTGTGACTACATCGGGGCTTGCAAATACATCCCCCTTGCCTGGACTCTGAGCTGACC 540
QY 541 GAATTTCCCTTGGCGCATGCGGACTGGCTCAAGAACTGCTGTGTGCTGCTGATGAGAGG 600
Db 541 GAATTTCCCTTGGCGCATGCGGACTGGCTCAAGAACTGCTGTGTGCTGATGAGAGG 600
QY 601 GATGAGGACAACTTCTGTGACTGAGAGGAGCTGCGGGTGAAGAGATCCATGAG 660
Db 601 GATGAGGACAACTTCTGTGACTGAGAGGAGCTGCGGGTGAAGAGATCCATGAG 660
QY 661 AATGAGAAGCGCTGGAGGAGGAGACACCCGTGAGCTGTGGCCGGGACTTCGAG 720
Db 661 AATGAGAAGCGCTGGAGGAGGAGACACCCGTGAGCTGTGGCCGGGACTTCGAG 720
QY 721 AAGAACTATAACATGTATCATCTTCCCTGTACACTGGCAGTTTGGCCAGCTGGACGAC 780
Db 721 AAGAACTATAACATGTATCATCTTCCCTGTACACTGGCAGTTTGGCCAGCTGGACGAC 780
QY 781 CCATTTGACGGGTACCTTCCACACCGAGCTGGCTCCACTGGTGTCCCTCATCCCC 840
Db 781 CCATTTGACGGGTACCTTCCACACCGAGCTGGCTCCACTGGTGTCCCTCATCCCC 840
QY 841 ATGAGCATTTGCAACACCCCTTTTTCGAGACCTGTGACCTGGCAATGACAACTGATC 900
Db 841 ATGAGCATTTGCAACACCCCTTTTTCGAGACCTGTGACCTGGCAATGACAACTGATC 900
QY 901 GCGCTGGATGAGTGGGCGGCTGCTTCGGCATCAAGCAGAGGATATCGAAGAGATCTT 960
Db 901 GCGCTGGATGAGTGGGCGGCTGCTTCGGCATCAAGCAGAGGATATCGAAGAGATCTT 960
QY 961 GTGATCTAAATCCACTCTTCCACAGTACCGGATCTCTTTTAAACCTCCCTTCCTGT 1020
Db 961 GTGATCTAAATCCACTCTTCCACAGTACCGGATCTCTTTTAAACCTCCCTTCCTGT 1020
QY 1021 TTCCCCCAATGTTTAAATGTTTGGATGTTTGTGTTCTGCTCGGAGACAAGGTGCTAA 1080
Db 1021 TTCCCCCAATGTTTAAATGTTTGGATGTTTGTGTTCTGCTCGGAGACAAGGTGCTAA 1080
QY 1081 CATAGATTAAAGTGAATATCAATTAAACCGTGTCTAAATGAAAAATCTAACCAAGCATGA 1140
Db 1081 CATAGATTAAAGTGAATATCAATTAAACCGTGTCTAAATGAAAAATCTAACCAAGCATGA 1140
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Qy	361	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	420
Db	361		
Qy	421	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	420
Db	421		
Qy	481	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	480
Db	481		
Qy	541	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	480
Db	541		
Qy	601	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	540
Db	601		
Qy	661	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	600
Db	661		
Qy	721	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	600
Db	721		
Qy	781	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	660
Db	781		
Qy	841	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	720
Db	841		
Qy	901	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	720
Db	901		
Qy	961	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	780
Db	961		
Qy	1021	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	780
Db	1021		
Qy	1081	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	840
Db	1081		
Qy	1141	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	840
Db	1141		
Qy	1201	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	900
Db	1201		
Qy	1261	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	900
Db	1261		
Qy	1321	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	960
Db	1321		
Qy	1381	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	960
Db	1381		
Qy	1441	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	1020
Db	1441		
Qy	1501	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	1020
Db	1501		
Qy	1561	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	1080
Db	1561		
Qy	1621	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	1080
Db	1621		
Qy	1681	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	1140
Db	1681		
Qy	1741	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	1140
Db	1741		
Qy	1801	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	1200
Db	1801		
Qy	1861	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	1200
Db	1861		
Qy	1921	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	1260
Db	1921		
Qy	1981	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	1260
Db	1981		
Qy	2041	CCAGCCCCCATTTGGCGAGTTTGAGAAAGGTGTGCAGCAATGACAAACAGACCTTTCGACTCT	1320
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Qy	1681	GGAAGTGGTCAGCGCATCTCGCAGGGCTTCTCTCTCTGTCTTTTTGGAGAACACAGGGCT	1740
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XX	
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PA	(NECA-) NETHERLANDS CANCER INST.
PA	



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Search completed: May 9, 2005, 22:26:53  
Job time : 1078 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2005, 00:56:13 ; Search time 4544 Seconds  
(without alignments)  
2870.240 Million cell updates/sec

Title: US-09-340-595A-1  
Perfect score: 2133  
Sequence: 1 cgggagagcgctgtgctt.....aaaaaaaaaaaaaaaaaaaaa 2133

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 5654200 seqs, 3057283753 residues

Total number of hits satisfying chosen parameters: 11308400

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 22:26:58 ; Search time: 2435 Seconds  
(without alignments)  
1801.979 Million cell updates/sec

Title: US-09-340-595A-1  
Perfect score: 2133  
Sequence: 1 cggagagcgctctgcct.....aaaaaaaaaaaaaaaaaaaa 2133

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9398789 seqs, 102855566 residues

Total number of hits satisfying chosen parameters: 18797578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2133	100.0	2133	6	AX409444	AX409444 Sequence
5	2133	100.0	2133	6	AX775122	AX775122 Sequence
6	2133	100.0	2133	6	AX779822	AX779822 Sequence
7	2133	100.0	2133	9	HUMSPARC	J03040 Human SPARC
8	2110.8	99.0	2114	9	BC004974	BC004974 Homo sapi
9	2095	98.2	3178	9	BC072457	BC072457 Homo sapi
10	2079.2	97.5	2089	9	BC008011	BC008011 Homo sapi
11	2078	96.9	2128	6	AX302081	AX302081 Sequence
12	2066.8	96.9	2081	6	CQ728077	CQ728077 Sequence
13	2001.4	93.8	5347	6	AX747785	AX747785 Sequence
14	2001.4	93.8	5347	9	AK092877	AK092877 Homo sapi
15	1841	86.3	2035	6	AX834481	AX834481 Sequence
16	1841	86.3	2035	9	AK096969	AK096969 Homo sapi
17	1795.4	84.2	3815	6	CQ414584	CQ414584 Sequence
18	1388.6	65.1	2141	4	BOVOSTRA	J03233 Bovine oste
19	1304	61.1	1516	6	BD204659	BD204659 Human nuc

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DB	301		
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DB	361		
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DB	541		
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DB	781		
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DB	841		
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SOURCE	Homo sapiens (human)		
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REFERENCE	1		







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Qy	1381		GGGCTTCCCAGGTGGCTGGAGGTGGCAAGGGAAGTAACAGACACAGATGTTGTCA	1440
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Qy	1621		TTTCTTTTTCATATGAGCTGTGTTGTTCAAACTTTTGGAGCACGAGCTGTCAAGTCTCTG	1680
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Qy	1681		GGAAATGTCAGCGCATCCTCGAGGCTTCTCTCTCTGTCTTTTGGAGAACCGAGGCT	1740
Db	1681		GGAAATGTCAGCGCATCCTCGAGGCTTCTCTCTCTGTCTTTTGGAGAACCGAGGCT	1740
Qy	1741		CTTCTCAGGGCTCTAGGGACTGCCAGCTGTTTCAGCGAGGAAGGCCAAAATCAAGAGT	1800
Db	1741		CTTCTCAGGGCTCTAGGGACTGCCAGCTGTTTCAGCGAGGAAGGCCAAAATCAAGAGT	1800
Qy	1801		GAGATGTAGAAGTTGTAAATAGAAAAGTGGAGTTGGTGAATCGGTTGTTCTTCTCTC	1860
Db	1801		GAGATGTAGAAGTTGTAAATAGAAAAGTGGAGTTGGTGAATCGGTTGTTCTTCTCTC	1860
Qy	1861		ACATTTGGATGATGTCTATAAGGTTTTTGTAGCATGTTCTCTTTTCTCACCTTCCCCTT	1920
Db	1861		ACATTTGGATGATGTCTATAAGGTTTTTGTAGCATGTTCTCTTTTCTCACCTTCCCCTT	1920
Qy	1921		TGTTCTCTTATTAATCAAGAGAACTTCAAAAGTTAATGGGATGTCGAGTCTCACAGCT	1980
Db	1921		TGTTCTCTTATTAATCAAGAGAACTTCAAAAGTTAATGGGATGTCGAGTCTCACAGCT	1980
Qy	1981		GAGAACTCGTTCACCTCAAGCAATTCATGAAAAGCTGCTCTTATTAATCATACAAC	2040
Db	1981		GAGAACTCGTTCACCTCAAGCAATTCATGAAAAGCTGCTCTTATTAATCATACAAC	2040
Qy	2041		TCTCACCATGATGTGAAGATTTTCACAATCTTTTCAAAATAAAAAGTAATGACTTAGAAA	2100

[illegible]



QY 601 GATAGGACAAACCTTCTGACTGAGAGCAGAGAGCTGCGGTGAGAGAGATCCATGAG 660  
DB 601 GATAGGACAAACCTTCTGACTGAGAGCAGAGAGCTGCGGTGAGAGAGATCCATGAG 660  
QY 661 AATGAGAGCGCTGAGAGCAGAGAGACACCCCGTGGAGCTGCTGGCCCGGAGCTTCGAG 720  
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DB 1021 TTCCCCCAATGTTAAATGTTTGGATGTTTGGTGTGCTGCTGGAGCAAGGCTGCTAA 1080  
QY 1081 CATAGATTTAAGTGAATACATTAACCGTCTAAATGAATGAATCTTAACCCAGACATGA 1140  
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DB 1921 TGTCTTCTTATTAATCAAGAGAACTTCAAGTAAATGGGATGGTGGATCTCACAGGCT 1980  
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## RESULT 6

AX779822 AX779822 2133 bp DNA linear PAT 14-JUL-2003  
LOCUS Sequence 1979 from Patent WO03039443.  
DEFINITION AX779822  
ACCESSION AX779822  
VERSION AX779822.1 GI:32696816  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Haerlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S.,  
Dugas, M., Eils, R., Broers, B. and Mergenthaler, S.

TITLE Novel genetic markers for leukemias  
JOURNAL Patent: WO 03039443-A 1979 15-MAY-2003;  
Deutsches Krebsforschungszentrum (DE) ;  
Ludwig-Maximilian-Universitaet Muenchen (DE) ;  
PD, Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)

FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2133; DB 6; Length 2133;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2133; Conservative. 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGAGAGCGGCTCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 60  
DB 1 CGGAGAGCGGCTCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 60

QY 61 AGGCGCTCGATCTTCTTCTCTCTTCTCTCTTCTCTCTTCTCTCTTCTCTCTTCTCTCTTCT 120  
DB 61 AGGCGCTCGATCTTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCT 120

QY 121 GAAGCCCTGCTGATGAGACAGAGTGTGTGAAGAACTGTGGCAGAGGTGTACTGAGTGA 180

Db 121 GAAGCCCTGCTGATGAGACAGAGGTTGGTGAAGAACTGTGGCAGAGGTGACTGAGGTA 180  
Qy 181 TCTGTGGAGCTAATCTGTTCAGGTGGAAGTAGGAAATTTGATGATGTTGACAGAGGAA 240  
Db 181 TCTGTGGAGCTAATCTGTTCAGGTGGAAGTAGGAAATTTGATGATGTTGACAGAGGAA 240  
Qy 241 ACCGAAGAGGAGTGTGGCGGGAATTCCTGCCAGAACACCACTGCCAACAACCGGCAAG 300  
Db 241 ACCGAAGAGGAGTGTGGCGGGAATTCCTGCCAGAACACCACTGCCAACAACCGGCAAG 300  
Qy 301 GTGTGCAGCTGGATGAGAACCAACACCCCATGTGCGTGTGCCAGGACCCACCAAGCTGC 360  
Db 301 GTGTGCAGCTGGATGAGAACCAACACCCCATGTGCGTGTGCCAGGACCCACCAAGCTGC 360  
Qy 361 CCAGCCCCCATTTGGCAGTTTGAAGGTGTGACGCAATGACAAACAAGACTTTCGACTCT 420  
Db 361 CCAGCCCCCATTTGGCAGTTTGAAGGTGTGACGCAATGACAAACAAGACTTTCGACTCT 420  
Qy 421 TCCTGCCACTTCTTTGCCACCAAGTGCACCTGGAGGGCCACCAAGAGGGCCACAAGCTC 480  
Db 421 TCCTGCCACTTCTTTGCCACCAAGTGCACCTGGAGGGCCACCAAGAGGGCCACAAGCTC 480  
Qy 481 CACCTGACTACATCGGGCCCTTGCAATATACATCCCCCTTGGCCTGGACTCTGAGCTGACC 540  
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Qy 1081 CATAGATTTAAGTGAATACATTAACGGTGTAAATAATGAAATTTCTAACCCAGACATGA 1140  
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Qy 1321 AACTTAATACCTACCGAGTCAAGACTTTGTGTTCATTTTCAATTTCAAGGCTTTGGCTGCTGT 1380  
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Qy 1381 GGGCTTCCCGAGTGGCTGGAGTGGGCAAGGAAAGTAACAGACACACAGATGTTGTCA 1440  
Db 1381 GGGCTTCCCGAGTGGCTGGAGTGGGCAAGGAAAGTAACAGACACACAGATGTTGTCA 1440  
Qy 1441 AGATGTTTGGGATAGAGGCTCAGTGTGGAGAGATCCCTGCAAGATCCACCAACC 1500  
Db 1441 AGATGTTTGGGATAGAGGCTCAGTGTGGAGAGATCCCTGCAAGATCCACCAACC 1500  
Qy 1501 AGAAGCTGGTTCCTGAGGCTGTAACTGAGAGAAAGATTTCTGGGCTGTCTTATGAAA 1560  
Db 1501 AGAAGCTGGTTCCTGAGGCTGTAACTGAGAGAAAGATTTCTGGGCTGTCTTATGAAA 1560  
Qy 1561 TATAGACATTTCTACATAAGCCAGTTTCATCACCATTTCCTCTTACCTTTCAAGTGCAG 1620  
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Qy 2101 CTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA 2133  
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## RESULT 7

## HUMSPARC

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

HUMSPARC 2133 bp mRNA linear PRI 13-JAN-1995  
Human SPARC/osteonectin mRNA, complete cds.

J03040

GI:338312

calcium-binding protein; glycoprotein; osteonectin.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.





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QY 188 GAGCTAAATCTCTGCTCAGGTGGAGGTAGAGAAATTTGATGATGGTGAGAGAAACCGAAG 247  
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QY 181 GAGCTAAATCTCTGCTCAGGTGGAGGTAGAGAAATTTGATGATGGTGAGAGAAACCGAAG 240  
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DB |||||  
QY 1868 GATGATTTGTCATAAGGTTTGTAGCATGTTCTCTCTTTTCTTCCACCTCCCTTTTCTT 1927  
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QY 1861 GATGATTTGTCATAAGGTTTGTAGCATGTTCTCTCTTTTCTTCCACCTCCCTTTTCTT 1920  
DB |||||  
QY 1928 CTATTAATCAAGAGAACTTCAAAATGTTAATGGGATGGTGGATCTCAGGCTGAGAACT 1987  
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DB |||||  
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## RESULT 9

BC072457

LOCUS

DEFINITION

Homo sapiens secreted protein, acidic, cysteine-rich (osteonectin),

mRNA (cdna clone MGC:88065 IMAGE:618668), complete cds.

ACCESSION

BC072457

VERSION

BC072457.1

KEYWORDS

MGC.

BC072457 3178 bp mRNA linear PRI 30-JUN-2004

Homo sapiens secreted protein, acidic, cysteine-rich (osteonectin),

mRNA (cdna clone MGC:88065 IMAGE:618668), complete cds.

BC072457

BC072457.1

GI:47938228

















QY 385 AAGGTGTCAGCAATGACACAGACCTTCGACTCTTCTGCGCACTCTTTGCGCAAAAG 444  
Db 3629 AAGGTGTCAGCAATGACACAGACCTTCGACTCTTCTGCGCACTCTTTGCGCAAAAG 3688  
QY 445 TGCACCTTGGAGGCGCACCAAGAGGGGCACAAGCTCCACCTGGAGTACTCATCGGCGCTTGC 504  
Db 3689 TGCACCTTGGAGGCGCACCAAGAGGGGCACAAGCTCCACCTGGAGTACTCATCGGCGCTTGC 3748  
QY 505 AAATACATCCCCCTTGCCTGAGCTCTGAGCTGACCGAAATTCGCCCTGCGCATGCGGGAC 564  
Db 3749 AAATACATCCCCCTTGCCTGAGCTCTGAGCTGACCGAAATTCGCCCTGCGCATGCGGGAC 3808  
QY 565 TGGCTCAAGAACGTCCTGCTGCTCACCCTGTATGAGAGGGATGAGGACACAACTTCTGACT 624  
Db 3809 TGGCTCAAGAACGTCCTGCTGCTCACCCTGTATGAGAGGGATGAGGACACAACTTCTGACT 3868  
QY 625 GAGAAGCAGAACGTCGCGGTGGAAGAATCATCAGAAATGAGAAGCGCTGGAGCGAGGA 684  
Db 3869 GAGAAGCAGAACGTCGCGGTGGAAGAGATCATCAGAAATGAGAAGCGCTGGAGCGAGGA 3928  
QY 685 GACCACCCGCTGGAGCTGCTGCGCGGAGCTTCGAGAAGAACTATAACATGATCATCTTC 744  
Db 3929 GACCACCCGCTGGAGCTGCTGCGCGGAGCTTCGAGAAGAACTATAACATGATCATCTTC 3988  
QY 745 CCTGTACACTGGCAGTTCCGCCAGCTGGACAGCACCCCATTTGACGGGTACCTCTCCAC 804  
Db 3989 CCTGTACACTGGCAGTTCCGCCAGCTGGACAGCACCCCATTTGACGGGTACCTCTCCAC 4048  
QY 805 ACCGAGCTGGCTCCACTGCGTGTCTCCCTCATCCCATGGAGCATTCGACCCCGCTTT 864  
Db 4049 ACCGAGCTGGCTCCACTGCGTGTCTCCCTCATCCCATGGAGCATTCGACCCCGCTTT 4108  
QY 865 TTCGAGACCTGTGACCTGGACAATGACAAGTACATCGCCCTGGATGAGTGGCGGCTGC 924  
Db 4109 TTCGAGACCTGTGACCTGGACAATGACAAGTACATCGCCCTGGATGAGTGGCGGCTGC 4168  
QY 925 TTCGGCATCAGCAGAGGATATCGACAGGATCTGTGATCTAAATCCACTCTCCAC 984  
Db 4169 TTCGGCATCAGCAGAGGATATCGACAGGATCTGTGATCTAAATCCACTCTCCAC 4228  
QY 985 AGTACCGGATCTCTCTTTAAACCTCCCTTCGTGTCTCCCCCAATGTTTAAATGTTG 1044  
Db 4229 AGTACCGGATCTCTCTTTAAACCTCCCTTCGTGTCTCCCCCAATGTTTAAATGTTG 4288  
QY 1045 GATGTTGTTGTTCTGCTCGGACAGAGGTGCTAAACATAGATTAAGTAATACATTA 1104  
Db 4289 GATGTTGTTGTTCTGCTCGGACAGAGGTGCTAAACATAGATTAAGTAATACATTA 4348  
QY 1105 CGGTGCTAAATAAGAAATCTTAACCAAGACATGACATCTTACGCTGAACCTTAACTAT 1164  
Db 4349 CGGTGCTAAATAAGAAATCTTAACCAAGACATGACATCTTACGCTGAACCTTAACTAT 4408  
QY 1165 TAAGGCTTTTCCACAGCATTAAATAGTCCCATTTTCTGTGCAATTTGAGCTTTGCC 1224  
Db 4409 TAAGGCTTTTCCACAGCATTAAATAGTCCCATTTTCTGTGCAATTTGAGCTTTGCC 4468  
QY 1225 CATGCTTTATGGAACATGGGTGACAGGATCTGTGGCTCTGCGCTTAAACACACAT 1284  
Db 4469 CATGCTTTATGGAACATGGGTGACAGGATCTGTGGCTCTGCGCTTAAACACACAT 4528  
QY 1285 TGCAGCTTCAACTTTTCTCTTTAGTGTCTGTTGAAACTAAATCTTACCGAGTCAGACT 1344  
Db 4529 TGCAGCTTCAACTTTTCTCTTTAGTGTCTGTTGAAACTAAATCTTACCGAGTCAGACT 4588  
QY 1345 TTGTGTTTCATTTTCAAGGCTCTTGGCTGCTGCTGGGCTTCCCGAGTGGCGCTGGAGG 1404  
Db 4589 TTGTGTTTCATTTTCAAGGCTCTTGGCTGCTGCTGGGCTTCCCGAGTGGCGCTGGAGG 4648  
QY 1405 TGGGCAAGGGAAGTAACAGACACAGCATGTGTGTCAGGATGGTTTTGGGACTAGAGCT 1464  
Db 4649 TGGGCAAGGGAAGTAACAGACACAGCATGTGTGTCAGGATGGTTTTGGGACTAGAGCT 4708  
QY 1465 CAGTGGTGGGAGAGATCCCTGCAGAAATCCCAACCAAGACGTTGCTGGCTGAGGCTGT 1524

Db 4709 CAGTGGTGGGAGAGATCCCTGCAGAAACCCACCAACGAGACGTTGCTGAGGCTGT 4768  
QY 1525 AACCTGAGAGAAAGATCTGGGCTGTCTTATGAAAAATATAGACATTTCTCATAAGCCCA 1584  
Db 4769 AACCTGAGAGAAAGATCTGGGCTGTCTTATGAAAAATATAGACATTTCTCATAAGCCCA 4828  
QY 1585 GTTCATCACCATTTCTCTCTTACCTTTTCTGAGTGGATTTCTTTTTCATATTAGGCTGTGG 1644  
Db 4829 GTTCATCACCATTTCTCTCTTACCTTTTCTGAGTGGATTTCTTTTTCATATTAGGCTGTGG 4888  
QY 1645 TTCAAACCTTTTGGAGCACGAGCTGTCTGAGTCTCTGGAAGTGTCTGAGCGCATCTCTCAG 1704  
Db 4889 TTCAAACCTTTTGGAGCACGAGCTGTCTGAGTCTCTGGAAGTGTCTGAGCGCATCTCTCAG 4948  
QY 1705 GGCTTCTCTCTCTCTGTCTTTTGGAGAACGAGGCTCTTCTCAGGGGCTCTAGGAGCTGC 1764  
Db 4949 GGCTTCTCTCTCTCTGTCTTTTGGAGAACGAGGCTCTTCTCAGGGGCTCTAGGAGCTGC 5008  
QY 1765 CAGCTGTCTTTCAGCCAGGAAGGCCAAAATCAAGAGTGAGATGTAGAAAGTTGTAATAATAG 1824  
Db 5009 CAGCTGTCTTTCAGCCAGGAAGGCCAAAATCAAGAGTGAGATGTAGAAAGTTGTAATAATAG 5068  
QY 1825 AAAAAAGTGGAGTTGGTGAATCGGTTGTTCTTCTCACAATTTGGATGATTTGTCATAAGGT 1884  
Db 5069 AAAAAAGTGGAGTTGGTGAATCGGTTGTTCTTCTCACAATTTGGATGATTTGTCATAAGGT 5128  
QY 1885 TTTTAGCATGTTCTCTCTCTTCTTCCACCTCCCTTTGTTCTTCTTATTAATCAAGAGAA 1944  
Db 5129 TTTTAGCATGTTCTCTCTCTTCTTCCACCTCCCTTTTCTTCTTATTAATCAAGAGAA 5188  
QY 1945 CTTCAAAGTTAATGGAGTGTCTGATCTCAGCGCTGAGAACTCGTTCACTCCAAGCAT 2004  
Db 5189 CTTCAAAGTTAATGGAGTGTCTGATCTCAGCGCTGAGAACTCGTTCACTCCAAGCAT 5248  
QY 2005 TTTATGAAAAAGCTGCTTCTTATTAATCATACAAACTCTCACCATGATGTGAAGAGTTTC 2064  
Db 5249 TTTATGAAAAAGCTGCTTCTTATTAATCATACAAACTCTCACCATGATGTGAAGAGTTTC 5308  
QY 2065 ACAAACTTTTCAAAATAAAAGTAATGACTTAGAAACTG 2103  
Db 5309 ACAAACTTTTCAAAATAAAAGTAATGACTTAGAAACTG 5347

## RESULT 14

AK092877  
LOCUS Homo sapiens cDNA FLJ35558 fis, clone SPLEN2004984, highly similar to M.musculus mRNA for myosin I.  
DEFINITION AK092877  
ACCESSION AK092877  
VERSION AK092877.1 GI:21751578  
KEYWORDS oligo capping; fis (full insert sequence).  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagabari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Hirakawa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Oshima, A., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Mori, S., Momiyama, H., Satoh, N., Takami, S.,

Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, P., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takenoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hiroo, M., Ohmori, Y., Kawabata, A., Hiki, J., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs  
Nat. Genet. 36 (1), 40-45 (2004)

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## JOURNAL

## COMMENT

## FEATURES

## source

## CDS

VGDGLPKSSKPTRKGMKAPRRSSQAPTRAAPRPMGRMNRGVPPSARGGPLEIM  
 SGGGTHRRPGRPPSPSTLCSASRRPRPSEHNTEFLNVPDOGMQRKRSVGRPVP  
 GVGRPKPDRTHPRCRALYQYVGQDVEDLSFNVEVIELMEDPSGWWKRLHGQEG  
 LGSFARSAPA"  
 ORIGIN  
 Query Match 93.8%; Score 2001.4; DB 9; Length 5347;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 2008; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 QY 85 TCCCTGGCGGGAGGCGCTTGGCAGCCCTCAGCAAGAGCCCTCGCTGATGAGACAG 144  
 DB 3329 TTCACGGCCGAGAGGCGCTTGGCAGCCCTCAGCAAGAGCCCTCGCTGATGAGACAG 3388  
 QY 145 GTGGTGGAGAAACTGTGGCAGAGGTGACTGAGGTATCTGTGGGAGCTTAATCTGTCCAG 204  
 DB 3389 GTGGTGGAGAAACTGTGGCAGAGGTGACTGAGGTATCTGTGGGAGCTTAATCTGTCCAG 3448  
 QY 205 GTGGAGGTAGGAGAAATTTGATGATGCTGAGAGAAACCGAAGAGAGGTGTGTGGCGGAA 264  
 DB 3449 GTGGAGGTAGGAGAAATTTGATGATGCTGAGAGAAACCGAAGAGAGGTGTGTGGCGGAA 3508  
 QY 265 AATCCCTGCCAGAACCCACCTGCAACACCGCAAGGTGTGCGAGCTGATGAGACACAC 324  
 DB 3509 AATCCCTGCCAGAACCCACCTGCAACACCGCAAGGTGTGCGAGCTGATGAGACACAC 3568  
 QY 325 ACCCCCATGTGCTGTGCGAGGACCCACACAGCTGCCAGCCCTCCAGAGCTTGGAGTTGAG 384  
 DB 3569 ACCCCCATGTGCTGTGCGAGGACCCACACAGCTGCCAGCCCTCCAGAGCTTGGAGTTGAG 3628  
 QY 385 AAGGTGTGCGACCAATGACAAACAGACCTTTCGACTCTTCTGCGACCTTCTTTGCCACAAAG 444  
 DB 3629 AAGGTGTGCGACCAATGACAAACAGACCTTTCGACTCTTCTGCGACCTTCTTTGCCACAAAG 3688  
 QY 445 TGCACCTTGGAGGGGACCAAGAGGGGACCAAGCTTCCAGCTGAGTACATCGGGCTTGC 504  
 DB 3689 TGCACCTTGGAGGGGACCAAGAGGGGACCAAGCTTCCAGCTGAGTACATCGGGCTTGC 3748  
 QY 505 AAATACATCCCCCTTGGCTGAGCTCTGAGCTGACCGAATTCCTCCCTGCGCATGCGGGAC 564  
 DB 3749 AAATACATCCCCCTTGGCTGAGCTCTGAGCTGACCGAATTCCTCCCTGCGCATGCGGGAC 3808  
 QY 565 TGGCTCAAAGACGCTCTGCTGCTCAGCTGATGAGAGGGATGAGGACAAACCTTCTGACT 624  
 DB 3809 TGGCTCAAAGACGCTCTGCTGCTCAGCTGATGAGAGGGATGAGGACAAACCTTCTGACT 3868  
 QY 625 GAGAGCAGAGCTGCGGGTGAAGAGATCCATGAGATGAGAGCGCTGAGAGCAGGA 684  
 DB 3869 GAGAGCAGAGCTGCGGGTGAAGAGATCCATGAGATGAGAGCGCTGAGAGCAGGA 3928  
 QY 685 GACCACCCCTGGAGCTGCTGCGCGGACCTTCGAGAGAGAACTATAACATGTACATCTTC 744  
 DB 3929 GACCACCCCTGGAGCTGCTGCGCGGACCTTCGAGAGAGAACTATAACATGTACATCTTC 3988  
 QY 745 CCTGTACACTGGCAGTTCCGGCAGCTGGAACAGCAACCCCATTTGACGGGTACCTCTCCAC 804  
 DB 3989 CCTGTACACTGGCAGTTCCGGCAGCTGGAACAGCAACCCCATTTGACGGGTACCTCTCCAC 4048  
 QY 805 ACCGAGCTGGCTCCAGCTGCTGCTCCCTCATCCCATGGAGCATTCACACCCCGCTTT 864  
 DB 4049 ACCGAGCTGGCTCCAGCTGCTGCTCCCTCATCCCATGGAGCATTCACACCCCGCTTT 4108  
 QY 865 TTCGAGACCTGTGACCTGGACCAATGACAAAGTACATCGCCCTGGATGAGTGGCGCGGCTGC 924  
 DB 4109 TTCGAGACCTGTGACCTGGACCAATGACAAAGTACATCGCCCTGGATGAGTGGCGCGGCTGC 4168  
 QY 925 TTCGAGCAACAGAGAGGATATCGAAGAGATCTTGTGATCTAAATCCATCTCTTCCAC 984  
 DB 4169 TTCGAGCAACAGAGAGGATATCGAAGAGATCTTGTGATCTAAATCCATCTCTTCCAC 4228  
 QY 985 AGTACCGGATCTCTCTTTAAACCTCCCTCGGTTCCTCCCATGTTTAAATGTTT 1044  
 DB 4229 AGTACCGGATCTCTCTTTAAACCTCCCTCGGTTCCTCCCATGTTTAAATGTTT 4288





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QY 65 CCTGATCTTCTTCTCTTCCCTTGGCGGAGGCGCTTGGCAGCCCTCAGCAAGAAG 124  
DB 61 CCTGATCTTCTTCTCTTCCCTTGGCGGAGGCGCTTGGCAGCCCTCAGCAAGAAG 120  
QY 125 CCTGCTGATGAGACAGAGGTGGTGGAGAACTGTGGCAGAGTGTAGAGTATCTG 184  
DB 121 CCTGCTGATGAGACAGAGGTGGTGGAGAACTGTGGCAGAGTGTAGAGTATCTG 180  
QY 185 TGGGAGCTTAATCCTGCTCAGAGTGGAAAGTAGGAGAAATTTGATGATGGTGCAGAGGAAACCG 244  
DB 181 TGGGAGCTTAATCCTGCTCAGAGTGGAAAGTAGGAGAAATTTGATGATGGTGCAGAGGAAACCG 240  
QY 245 AAGAGAGGTGTGGCGGAAATCCTGTCAGAAACCAACCTGCAAAACAGGCAAGGTGT 304  
DB 241 AAGAGAGGTGTGGCGGAAATCCTGTCAGAAACCAACCTGCAAAACAGGCAAGGTGT 300  
QY 305 GCGAGCTGATGAGAACACACCCCTGATGAGTGGTGGCAGGACCCACAGCTGCCAG 364  
DB 301 GCGAGCTGATGAGAACACACCCCTGATGAGTGGTGGCAGGACCCACAGCTGCCAG 360  
QY 365 CCCCACTTGGCAGTTGAGAAAGTGTGAGCAATGACAAAGACCTTTGCACTCTTCT 424  
DB 361 CCCCACTTGGCAGTTGAGAAAGTGTGAGCAATGACAAAGACCTTTGCACTCTTCT 420  
QY 425 GCCACTTCTTGCACAAAGTGCACCTGGAGGGCACCAAGAGGGCCCAAGCTCCACC 484  
DB 421 GCCACTTCTTGCACAAAGTGCACCTGGAGGGCACCAAGAGGGCCCAAGCTCCACC 480  
QY 485 TGGACTACATCGGCGCTTGCNAATACATCCCTTGCCTGCTGACCTGAGCTGACCGAAT 544  
DB 481 TGGACTACATCGGCGCTTGCNAATACATCCCTTGCCTGCTGACCTGAGCTGACCGAAT 540  
QY 545 TCCCTCTGCGATGCGGAGCTGCTCAAGAACGTCCTGCTCACCTGATGAGAGGATG 604  
DB 541 TCCCTCTGCGATGCGGAGCTGCTCAAGAACGTCCTGCTCACCTGATGAGAGGATG 600  
QY 605 AGGACAAACCTTCTGACTGAGAGAGAGAGAGCTGGGTGAGAGATCCATGAGATG 664  
DB 601 AGGACAAACCTTCTGACTGAGAGAGAGAGAGCTGGGTGAGAGATCCATGAGATG 660  
QY 665 AGAGCGCTGAGGCGAGAGACCAACCGTGGAGCTGCTGCGGAGCTTTCGAGAAG 724  
DB 661 AGAGCGCTGAGGCGAGAGACCAACCGTGGAGCTGCTGCGGAGCTTTCGAGAAG 720  
QY 725 ACTATAACATGTACATCTTCCCTGTACACTGGCAGTTTCGCGCAGCTGACACCCCA 784  
DB 721 ACTATAACATGTACATCTTCCCTGTACACTGGCAGTTTCGCGCAGCTGACACCCCA 780  
QY 785 TTGACGGGTACCTCTCCACACCGAGCTGGCTCCACTGGTGTGCTCCCTCATCCCATGG 844  
DB 781 TTGACGGGTACCTCTCCACACCGAGCTGGCTCCACTGGTGTGCTCCCTCATCCCATGG 840  
QY 845 AGCATTGACACCCCGCTTTTCGAGACCTGTGACCTGGACAAATGACAGATGATCGCC 904  
DB 841 AGCATTGACACCCCGCTTTTCGAGACCTGTGACCTGGACAAATGACAGATGATCGCC 900  
QY 905 TGGATGAGTGGCGGCTGCTTCGGCATCAAGCAGAGGATATCGAAGGATCTTTGGA 964  
DB 901 TGGATGAGTGGCGGCTGCTTCGGCATCAAGCAGAGGATATCGAAGGATCTTTGGA 960  
QY 965 TCTAAATCCATCTCTTCCACAGTACCGGATCTCTCTTTAAACCTCCCTCTGTTTCC 1024  
DB 961 TCTAAATCCATCTCTTCCACAGTACCGGATCTCTCTTTAAACCTCCCTCTGTTTCC 1020  
QY 1025 CCCAATGTTTAAATGTTTGGATGTTTGTGTTGCTGCTGGAGACAGGTGCTAACATA 1084  
DB 1021 CCCAATGTTTAAATGTTTGGATGTTTGTGTTGTTCTGCTGGAGACAGGTGCTAACATA 1080  
QY 1085 GATTTAAGTGAATACATTAACCGTGTCTAAATGAAAAATTCATCCCAAGACATGACATT 1144  
DB 1081 GATTTAAGTGAATACATTAACCGTGTCTAAATGAAAAATTCATCCCAAGACATGACATT 1140

QY 1145 CTTAGCTGAACCTAACTATTAAAGCGCTTTTCCACAGCATTAAATAGTCCCATTTTCTC 1204  
DB 1141 CTTAGCTGAACCTAACTATTAAAGCGCTTTTCCACAGCATTAAATAGTCCCATTTTCTC 1200  
QY 1205 TTGCCATTGTAGCTTTTGGCCATTGTCTTATTGGCACAATGGGTGGACACGGATCTGCTGG 1264  
DB 1201 TTGCCATTGTAGCTTTTGGCCATTGTCTTATTGGCACAATGGGTGGACACGGATCTGCTGG 1260  
QY 1265 GCTCTGCTTAAACACACATTGCGAGCTTCAATTTCTCTTTAGTGTCTGTGTGAAACT 1324  
DB 1261 GCTCTGCTTAAACACACATTGCGAGCTTCAATTTCTCTTTAGTGTCTGTGTGAAACT 1320  
QY 1325 AATCTTACCAGTCAGACTTTGTTCATTTCTCAGGCTTGTGCTGCTGCTGGGC 1384  
DB 1321 AATCTTACCAGTCAGACTTTGTTCATTTCTCAGGCTTGTGCTGCTGCTGGGC 1380  
QY 1385 TTCCCAAGCTGGCCTGGAGGTGGGCAAGGAAAGTAAACAGACACACGATTTGTCAAGGA 1444  
DB 1381 TTCCCAAGCTGGCCTGGAGGTGGGCAAGGAAAGTAAACAGACACACGATTTGTCAAGGA 1440  
QY 1445 TGGTTTGGGACTAGAGGCTCAGTGGTGGGAGAGATCCCTGCGAGAAATCCACCAACAGAA 1504  
DB 1441 TGGTTTGGGACTAGAGGCTCAGTGGTGGGAGAGATCCCTGCGAGAAATCCACCAACAGAA 1500  
QY 1505 CGTGGTTTGGCCTGAGGCTGTAACCTGAGAGAAAGATTCTGGGCTGTCTTATGAAATATA 1564  
DB 1501 CGTGGTTTGGCCTGAGGCTGTAACCTGAGAGAAAGATTCTGGGCTGTCTTATGAAATATA 1560  
QY 1565 GACATTTCTCACAATAGCCAGTTCAATCACCATTTCCTCTTTTACCTTTTCACTGAGTTC 1624  
DB 1561 GACATTTCTCACAATAGCCAGTTCAATCACCATTTCCTCTTTTACCTTTTCACTGAGTTC 1620  
QY 1625 TTTTCAATAGGCTGTGGTTTCAAACTTTTGGAGACAGGACTGTCACTCTCTGGGA 1684  
DB 1621 TTTTCAATAGGCTGTGGTTTCAAACTTTTGGAGACAGGACTGTCACTCTCTGGGA 1680  
QY 1685 GTGGTCAGCGATCCTGCGAGGCTTCTCTCTCTGTCTTTTGGAGAACACAGGCTCTTC 1744  
DB 1681 GTGGTCAGCGATCCTGCGAGGCTTCTCTCTCTGTCTTTTGGAGAACACAGGCTCTTC 1740  
QY 1745 TCAGGGGCTTAGGGACTGCCAGGCTGTTTTCAGCCAGGAAGCCAAAATCAAGAGTGAGA 1804  
DB 1741 TCAGGGGCTTAGGGACTGCCAGGCTGTTTTCAGCCAGGAAGCCAAAATCAAGAGTGAGA 1800  
QY 1805 TGTAGAAAGTTGTAAATAGAAAAGTGGAGTGGTGAATCGGTTGTCTTCTCCATCAT 1864  
DB 1801 TGTAGAAAGTTGTAAATAGAAAAGTGGAGTGGTGAATCGGTTGTCTTCTCCATCAT 1860  
QY 1865 TTGGATGATGTGATAAGGTTTTCAGCATGTTTCTCTCTTTTTCACCTCCCTTTGTT 1924  
DB 1861 TTGGATGATGTGATAAGGTTTTCAGCATGTTTCTCTCTTTTTCACCTCCCTTTT 1920  
QY 1925 CTTCTATTAAATCAAGAGAACTTCAAGATTAATGGGATGGTGGATCTCACAGGCTGAGA 1984  
DB 1921 CTTCTATTAAATCAAGAGAACTTCAAGATTAATGGGATGGTGGATCTCACAGGCTGAGA 1980  
QY 1985 ACTCGTCACTCCAGCATTTTCATGAAAAGCTCTCTTATTATTAATCATACAACTCTC 2044  
DB 1981 ACTCGTCACTCCAGCATTTTCATGAAAAGCTCTCTTATTATTAATCATACAACTCTC 2040  
QY 2045 ACCATGATGTGAAGAGTTTTCACAAATCTTTCAAAAATAAAAAGTAATG 2091  
DB 2041 ACCATGATGTGAAGAGTTTTCACAAATCTTTCAAAAATAAAAAGTAATG 2087

## RESULT 2

CR626474

LOCUS

DEFINITION  
full-length cDNA clone CS0E012YG17 of Placenta of Homo sapiens (human).

ACCESSION

CR626474

VERSION

CR626474.1

GI:50507281

KEYWORDS

HTC; CNSLT\_cDNA.

2100 bp mRNA linear HTC 21-JUL-2004







Qy	481	CACCTGACATACATCGGGCCCTTGCAAAATACATCCCCCTTGCTCTGGACTCTGAGCTGAC	540
Db	500	CACCTGACATACATCGGGCCCTTGCAAAATACATCCCCCTTGCTCTGGACTCTGAGCTGAC	559
Qy	541	GAATTCCTCCCTGCGCATGCGGGACTGGCTCAAGAAACGTCTCGTTCACCCCTGTATGAGAG	600
Db	560	GAATTCCTCCCTGCGCATGCGGGACTGGCTCAAGAAACGTCTCGTTCACCCCTGTATGAGAG	619
Qy	601	GATGAGGACAAACACTTCTGACTGAGAAGCAGAAAGCTGCGGTGAAGAAAGATCCATGAG	660
Db	620	GATGAGGACAAACACTTCTGACTGAGAAGCAGAAAGCTGCGGTGAAGAAAGATCCATGAG	679
Qy	661	AATGAGAAGCGCCTGGAGGACGAGACCAACCCCGTGGAGCTGCTGGCCCGGGAATTCGAG	720
Db	680	AATGAGAAGCGCCTGGAGGACGAGACCAACCCCGTGGAGCTGCTGGCCCGGGAATTCGAG	739
Qy	721	AAGAACTATAACATGTACATCTTCCCTGTACACTGGCAGTTTCGGCAGCTGGACACGAC	780
Db	740	AAGAACTATAACATGTACATCTTCCCTGTACACTGGCAGTTTCGGCAGCTGGACACGAC	799
Qy	781	CCCAATTCAGCGGTACCTCTCCACACCGAGCTGCTCCACTGGCTGCTCCCTCATCCCC	840
Db	800	CCCAATTCAGCGGTACCTCTCCACACCGAGCTGCTCCACTGGCTGCTCCCTCATCCCC	859
Qy	841	ATGAGCAATTGCACACACCGCTTTTTCGAGACCTGTGACCTGGACAATGACAAGTACATC	900
Db	860	ATGAGCAATTGCACACACCGCTTTTTCGAGACCTGTGACCTGGACAATGACAAGTACATC	919
Qy	901	GCCCTGANTGAGTGGCGCGCTGCTTCGGCATCAAGCAGAAGATTCGACAAGATCTTT	960
Db	920	GCCCTGANTGAGTGGCGCGCTGCTTCGGCATCAAGCAGAAGATTCGACAAGATCTTT	979
Qy	961	GTGATCTAAATCCACTCCTTCCACAGTACCGGATCTCTCTTTAAACCTCCCTTCGTGT	1020
Db	980	GTGATCTAAATCCACTCCTTCCACAGTACCGGATCTCTCTTTAAACCTCCCTTCGTGT	1039
Qy	1021	TTCCCCCAATGTTTAAATGTTTGGATGGTTGTTGTTCTGCTCGGAGACAAGTGCTAA	1080
Db	1040	TTCCCCCAATGTTTAAATGTTTGGATGGTTGTTGTTCTGCTCGGAGACAAGTGCTAA	1099
Qy	1081	CATGATTTTAAGTGAATACATTAAACGGTGTAAATAATGAAATTTCTAAACCAAGACATG	1140
Db	1100	CATGATTTTAAGTGAATACATTAAACGGTGTAAATAATGAAATTTCTAAACCAAGACATG	1159
Qy	1141	CATTCTTAGCTGAACCTTAACTATTAAAGGCCCTTTCCACAGCATTAATAGTCCCATTTT	1200
Db	1160	CATTCTTAGCTGAACCTTAACTATTAAAGGCCCTTTCCACAGCATTAATAGTCCCATTTT	1219
Qy	1201	TCTCTTGCCATTGTAGCTTTGCCCATTTGTCATTATGGCACAATGGGTGGACACGGATCTG	1260
Db	1220	TCTCTTGCCATTGTAGCTTTGCCCATTTGTCATTATGGCACAATGGGTGGACACGGATCTG	1279
Qy	1261	CTGGGCTCTGCTTAAACACACATTCGAGCTTCAACTTTCTTTTATGTTGTTCTGTTTGA	1320
Db	1280	CTGGGCTCTGCTTAAACACACATTCGAGCTTCAACTTTCTTTTATGTTGTTCTGTTTGA	1339
Qy	1321	AACCTAACTTACCGAGTCAGACTTGTGTTCATTCTTCAATTCAGGGTCTTGGCTGCCTGT	1380
Db	1340	AACCTAACTTACCGAGTCAGACTTGTGTTCATTCTTCAATTCAGGGTCTTGGCTGCCTGT	1399
Qy	1381	GGGCTTCCCCAGGTGGCCTGGAGGTGGGCAAGGAAAGTAAACAGACACACGATGTTGCA	1440
Db	1400	GGGCTTCCCCAGGTGGCCTGGAGGTGGGCAAGGAAAGTAAACAGACACACGATGTTGCA	1459
Qy	1441	AGGATGTTTTGGACTAGAGGCTCAGTGGTGGGAGAGATCCCTGCAAGATTCACCAACC	1500
Db	1460	AGGATGTTTTGGGACTAGAGGCTCAGTGGTGGGAGAGATCCCTGCAAGATTCACCAACC	1519
Qy	1501	AGAACGTGTTTGCTCGAGGCTGTAACTGAGAGAAAGATTTCTGGGGCTGTCTTATGAAA	1560
Db	1520	AGAACGTGTTTGCTCGAGGCTGTAACTGAGAGAAAGATTTCTGGGGCTGTCTTATGAAA	1579
Qy	1561	TATAGACATTTCTCATAAAGCCCAAGTTTCATCACCATTTCCTTTTACCTTTTCAAGTCAG	1620

[illegible]











907	Db	 GCCCTGATGAGTGGGCGGCTGTTTCGGCATCAAAGCAGAAGGATATCGACAAGGATCTT	966
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967	Db	GTGATCTAAATCCACTCTCTTCCACAGTACCGGATCTCTCTTTAAACCTCCCTCGTGT	1026
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1147	Db	CATTCTTAGCTGTAACTTAATATTAAGGCGCTTTTCCACAGCATTAATAGTCCCATTTT	1206
1201	Qy	TCTCTGGCATTTGTAGCTTTGCCATTTGCTTTATTGGCACATGGGTGGACACGGATCTG	1260
1207	Db	TCTCTGGCATTTGTAGCTTTGCCATTTGCTTTATTGGCACATGGGTGGACACGGATCTG	1266
1261	Qy	CTGGGCTCTGCCTTAAACACACATTTGAGCTTCAACTTTTCTCTTTAGTGTCTGTTTGA	1320
1267	Db	CTGGGCTCTGCCTTAAACACACATTTGAGCTTCAACTTTTCTCTTTAGTGTCTGTTTGA	1326
1321	Qy	AACATAACTTACCGAGTCAGACTTTGTGTTTCATTTTCATTCAGGGTCTGGGCTGCTGT	1380
1327	Db	AACATAACTTACCGAGTCAGACTTTGTGTTTCATTTTCATTCAGGGTCTGGGCTGCTGT	1386
1381	Qy	GGGCTTCCCCAGGTGGCTGGAGGTGGCAAGGGAAGTAACAGACACACGATGTTGTCA	1440
1387	Db	GGGCTTCCCCAGGTGGCTGGAGGTGGCAAGGGAAGTAACAGACACACGATGTTGTCA	1446
1441	Qy	AGGATGGTTTTGGACTAGAGGCTCAGTGGTGGAGAGATCCCTGCGAGAATCCACCAACC	1500
1447	Db	AGGATGGTTTTGGACTAGAGGCTCAGTGGTGGAGAGATCCCTGCGAGAATCCACCAACC	1506
1501	Qy	AGAACGTGGTTTGCTCAGGCTGTAACTGAGAGAAAAGATTCGGGGCTGCTTATGAAAA	1560
1507	Db	AGAACGTGGTTTGCTCAGGCTGTAACTGAGAGAAAAGATTCGGGGCTGCTTATGAAAA	1566
1561	Qy	TATAGACATCTCACATAAGCCAGTTCATCACCATTTCCTCCTTTACCTTTTCAGTGCAG	1620
1567	Db	TATAGACATCTCACATAAGCCAGTTCATCACCATTTCCTCCTTTTCAGTGCAG	1626
1621	Qy	TTTCTTTTTCATATTAGGCTGTGGTTTCAAACTTTTGGGAGCACGGACTGTCAGTTCTCTG	1680
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1681	Qy	GGAGTGGTTCAGCGCATCTCGAGGCTTCTCCTCCTCTGCTTTTCGAGAACCGAGGCT	1740
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1741	Qy	CTTCTCAGGGCTCTCAGGGACTGCCAGCTGTTTTTCAGCCAGGAAGGCCAAAATCAAGAGT	1800
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1801	Qy	GAGATGTAGAAAAGTTGTAAAAATAGAAAAAGTGGATTTGGTGAATTCGGTTGTTTCTTCCTC	1860
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2047 TCTCAGCATGATGAGAGTT 2068

RESULT 9  
CR604100  
LOCUS  
DEFINITION  
full-length cDNA clone CS0D011VH01 of Placenta of Homo sapiens (human)  
ACCESSION  
CR604100  
VERSION  
CR604100.1  
KEYWORDS  
HTC; CNSLT\_cDNA.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 2071)  
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 2071)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES  
SOURCE

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/db_xref="taxon:9606"
/clone="CS0DE011YH0"
/tissue_type="Placenta"
/plasmid="pCMVSPORT"

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## ORIGIN

Query Match 96.4%: Score 2055.6: DB 3: Length 2071;

Query Match 96.4%; SCORE 2055.6; DB 3; length 2071;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2058: Conservative 0: Mismatches 4: Indels 0: Gaps 0;

[illegible]









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Db	187		
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Db	247		
Qy	301	GTGTGCCAGCTGGATGATGAACAACACCCCATGTGGCTGTGCCAGGACCCCAACCAAGCTGC	360
Db	307		
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Db	427		
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Qy	721	AAGAACTATAACATGTATACATCTTCCCTGTATACACTGGCAGTTCGCGCCAGCTGGACCAAGCAC	780
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Qy	961	GTGATCTAAATCCACTCTTCCACAGTACCGGATCTCTCTTTAAACCTCCCTTGTGTGT	1020
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Qy	1021	TTCCCCCAATCTTTTAAATGTTTGGATGTTTGTGTGTCTGCTCGCTGGAGACAAAGTGTCTAA	1080
Db	1027	TTCCCCCAATGTTTAAATGTTTGGATGTTTGTGTGTCTGCTCGCTGGAGACAAAGTGTCTAA	1086
Qy	1081	CATAGATTTAAGTGAATACATTAAACGGTGTCTAAATAATGAAATTTCTAAACCAAGACATGA	1140
Db	1087	CATAGATTTAAGTGAATACATTAAACGGTGTCTAAATAATGAAATTTCTAAACCAAGACATGA	1146
Qy	1141	CATTCTTAGCTGTAACTTAACTATTAAAGCCCTTTTCCACAGCATTAATAGTCCCATTTT	1200
Db	1147	CATTCTTAGCTGTAACTTAACTATTAAAGCCCTTTTCCACAGCATTAATAGTCCCATTTT	1206
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Db	1207	TCTCTTGCCATTTGTAGCTTTGGCCATTGCTTAATGGGCATCATGGGTGGACACGATCTG	1266
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[illegible]

RESULT 13	
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ACCESSION	CR613247
VERSION	CR613247.1 GI:50494054
KEYWORDS	HTC; CNSLT_CDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 2080)
AUTHORS	Li,W.B., Gruber,C., Jesse,J., and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL :

REMARK  
Contact : Feng Liang Email : fliang@lifetech.com URL :









Db 661 |||||CGGCGGAGCTT||CGAGAGAACTAT||AACTGTAATCTTCCCTGTACACTGGCAGTTC 720  
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